```
   1 CGGTGCTGCC GGGCTCAGCC CCGTCTCCTC CTCTTGCTCC CTCGGCCGGG
  51 CGGCGGTGAC TGTGCACCGA CGTCGGCGCG GGCTGCACCG CCGCGTCCGC
 101 CCGCCCGCCA GCATGGCCAC CACCGCCACC TGCACCCGTT TCACCGACGA
 151 CTACCAGCTC TTCGAGGAGC TTGGCAAGGG TGCTTTCTCT GTGGTCCGCA
 201 GGTGTGTGAA GAAAACCTCC ACGCAGGAGT ACGCAGCAAA AATCATCAAT
 251 ACCAAGAAAT TGTCTGCCCG GGATCACCAG AAACTAGAAC GTGAGGCTCG
 301 GATATGTCGA CTTCTGAAAC ATCCAAACAT CGTGCGCCTC CATGACAGTA
 351 TTTCTGAAGA AGGGTTTCAC TACCTCGTGT TTGACCTGT TACCGGCGGG
 401 GAGCTGTTTG AAGACATTGT GGCCAGAGAG TACTACAGTG AAGCAGATGC
 451 CAGCCACTGT ATACATCAGA TTCTGGAGAG TGTTAACCAC ATCCACCAGC
 501 ATGACATCGT CCACAGGGAC CTGAAGCCTG AGAACCTGCT GCTGGCGAGT
 551 AAATGCAAGG GTGCCGCCGT CAAGCTGGCT GATTTTGGCC TAGCCATCGA
 601 AGTACAGGGA GAGCAGCAGG CTTGGTTTGG TTTTGCTGGC ACCCCAGGTT
 651 ACTTGTCCCC TGAGGTCTTG AGGAAAGATC CCTATGGAAA ACCTGTGGAT
 701 ATCTGGGCCT GCGGGGTCAT CCTGTATATC CTCCTGGTGG GCTATCCTCC
 751 CTTCTGGGAT GAGGATCAGC ACAAGCTGTA TCAGCAGATC AAGGCTGGAG
 801 CCTATGATTT CCCATCACCA GAATGGGACA CGGTAACTCC TGAAGCCAAG
 851 AACTTGATCA ACCAGATGCT GACCATAAAC CCAGCAAAGC GCATCACGGC
 901 TGACCAGGCT CTCAAGCACC CGTGGGTCTG TCAACGATCC ACGGTGGCAT
 951 CCATGATGCA TCGTCAGGAG ACTGTGGAGT GTTTGCGCAA GTTCAATGCC
1001 CGGAGAAAAC TGAAGGGTGC CATCCTCACG ACCATGCTTG TCTCCAGGAA
1051 CTTCTCAGTT GGCAGGCAGA GCTCCGCCCC CGCCTCGCCT GCCGCGAGCG
1101 CCGCCGGCCT GGCCGGGCAA GCTGCCAAAA GCCTATTGAA CAAGAAGTCG
1151 GATGGCGGTG TCAAGAAAAG GAAGTCGAGT TCCAGCGTGC ACCTAATGGA
1201 GCCACAAACC ACTGTGGTAC ACAACGCTAC AGATGGGATC AAGGGCTCCA
1251 CAGAGAGCTG CAACACCACC ACAGAAGATG AGGACCTCAA AGCTGCCCCG
1301 CTCCGCACTG GGAATGGCAG CTCGGTGCCT GAAGGACGGA GCTCCCGGGA
1351 CAGAACAGCC CCCTCTGCAG GCATGCAGCC CCAGCCTTCT CTCTGCTCCT
1401 CAGCCATGCG AAAACAGGAG ATCATTAAGA TTACAGAACA GCTGATTGAA
1451 GCCATCAACA ATGGGGACTT TGAGGCCTAC ACGAAGATTT GTGATCCAGG
1501 CCTCACTTCC TTTGAGCCTG AGGCCCTTGG TAACCTCGTG GAGGGGATGG
1551 ATTTCCATAA GTTTTACTTT GAGAATCTCC TGTCCAAGAA CAGCAAGCCT
1601 ATCCATACCA CCATCCTAAA CCCACACGTC CACGTGATTG GGGAGGACGC
1651 AGCGTGCATC GCCTACATCC GCCTCACCCA GTACATCGAC GGGCAGGGTC
1701 GGCCTCGCAC CAGCCAGTCA GAAGAGACCC GGGTCTGGCA CCGTCGGGAT
1751 GGCAAGTGGC TCAATGTCCA CTATCACTGC TCAGGGGCCC CTGCCGCACC
1801 GCTGCAGTGA GCTCAGCCAC AGGGGCTTTA GGAGATTCCA GCCGGAGGTC
1851 CAACCTTCGC AGCCAGTGGC TCTGGAGGGC CTGAGTGACA GCGGCAGTCC
1901 TGTTTGTTTG AGGTTTAAAA CAATTCAATT ACAAAGCGG CAGCAGCCAA
1951 TGCACGCCCC TGCATGCAGC CCTCCCGCCC GCCCTTCGTG TCTGTCTCTG
2001 CTGTACCGAG GTGTTTTTTA CATTTAAGAA AAAAAAAAA AAAAAAAAA
2051 AAAAAAAAA A  (SEQ ID NO:1)
```

FEATURES:
5'UTR: 1-112
Start Codon: 113
Stop Codon: 1808
3'UTR: 1811

Homologous proteins:
Top 10 BLAST Hits

		Score	E
CRA|88000001156376 /altid=gi|7434378 /def=pir||JC5636 Ca2+/calm...		1083	0.0
CRA|18000004937293 /altid=gi|125289 /def=sp|P11730|KCCG_RAT CAL...		1066	0.0
CRA|18000005054755 /altid=gi|1657464 /def=gb|AAC48714.1| (U7297...		1038	0.0
CRA|105000014644765 /altid=gi|10443740 /def=gb|AAG17558.1|AF233...		994	0.0
CRA|105000014644764 /altid=gi|10443738 /def=gb|AAG17557.1|AF233...		989	0.0
CRA|18000004903800 /altid=gi|422770 /def=pir||A46619 Ca2+/calmo...		986	0.0
CRA|18000005152785 /altid=gi|3241847 /def=dbj|BAA28869.1| (D149...		986	0.0
CRA|18000004937876 /altid=gi|631810 /def=pir||S43845 Ca2+/calmo...		985	0.0
CRA|18000004937877 /altid=gi|560653 /def=gb|AAB30671.1| (S71571...		984	0.0
CRA|105000014644762 /altid=gi|10443734 /def=gb|AAG17555.1|AF233...		976	0.0

FIGURE 1A

BLAST dbEST Hits:

	Score	E
gi|12893350 /dataset=dbest /taxon=960...	1778	0.0
gi|12790010 /dataset=dbest /taxon=960...	1463	0.0
gi|10142161 /dataset=dbest /taxon=96...	1443	0.0
gi|10158540 /dataset=dbest /taxon=96...	1366	0.0
gi|12796371 /dataset=dbest /taxon=960...	1356	0.0
gi|12340179 /dataset=dbest /taxon=96...	1320	0.0
gi|9342125 /dataset=dbest /taxon=960...	1185	0.0
gi|12386814 /dataset=dbest /taxon=96...	1180	0.0
gi|12421686 /dataset=dbest /taxon=96...	1172	0.0
gi|12886387 /dataset=dbest /taxon=960...	1063	0.0

EXPRESSION INFORMATION FOR MODULATORY USE:
library source (from BLAST dbEST hits):
gi|12893350 Placenta
gi|12790010 breast
gi|10142161 Skin melanotic melanoma
gi|10158540 Ovary adenocarcinoma cell line
gi|12796371 breast
gi|12340179 Uterus leiomyosarcoma
gi|9342125 Lymph Burkitt's lymphoma
gi|12386814 Small Interstine duodenal adenocarcinoma
gi|12421686 Breast mammary adenocarcinoma
gi|12886387 placenta

Tissue Expression:
Human fetal whole brain

FIGURE 1B

```
  1 MATTATCTRF TDDYQLFEEL GKGAFSVVRR CVKKTSTQEY AAKIINTKKL
 51 SARDHQKLER EARICRLLKH PNIVRLHDSI SEEGFHYLVF DLVTGGELFE
101 DIVAREYYSE ADASHCIHQI LESVNHIHQH DIVHRDLKPE NLLLASKCKG
151 AAVKLADFGL AIEVQGEQQA WFGFAGTPGY LSPEVLRKDP YGKPVDIWAC
201 GVILYILLVG YPPFWDEDQH KLYQQIKAGA YDFPSPEWDT VTPEAKNLIN
251 QMLTINPAKR ITADQALKHP WVCQRSTVAS MMHRQETVEC LRKFNARRKL
301 KGAILTTMLV SRNFSVGRQS SAPASPAASA AGLAGQAAKS LLNKKSDGGV
351 KKRKSSSSVH IMEPQTIVVH NATDGIKGST ESCNTTTEDE DLKAAPLRTG
401 NGSSVPEGRS SRDRTAPSAG MQPQPSLCSS AMRKQEIIKI TEQLIEAINN
451 GDFEAYTKIC DPGLTSFEPE ALGNLVEGMD FHKFYFENLL SKNSKPIHTT
501 ILNPHVHVIG EDAACIAYIR LTQYIDGQGR PRTSQSEETR VWHRRDGKWL
551 NVHYHCSGAP AAPLQ   (SEQ ID NO:2)
```

FEATURES:
Functional domains and key regions:
[1] PDOC00001 PS00001 ASN_GLYCOSYLATION
N-glycosylation site

Number of matches: 4
```
        1     313-316 NFSV
        2     371-374 NATD
        3     384-387 NTTT
        4     401-404 NGSS
```

[2] PDOC00004 PS00004 CAMP_PHOSPHO_SITE
cAMP- and cGMP-dependent protein kinase phosphorylation site

Number of matches: 5
```
        1      33-36  KKTS
        2      48-51  KKLS
        3     259-262 KRIT
        4     352-355 KRKS
        5     353-356 RKSS
```

[3] PDOC00005 PS00005 PKC_PHOSPHO_SITE
Protein kinase C phosphorylation site

Number of matches: 3
```
        1      47-49  TKK
        2      51-53  SAR
        3     410-412 SSR
```

[4] PDOC00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site

Number of matches: 12
```
        1      36-39  STQE
        2      51-54  SARD
        3      79-82  SISE
        4      94-97  TGGE
        5     109-112 SEAD
        6     385-388 TTTE
        7     386-389 TTED
        8     387-390 TEDE
        9     404-407 SVPE
       10     410-413 SSRD
       11     465-468 TSFE
       12     534-537 SQSE
```

[5] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

FIGURE 2A

Number of matches: 4
     1   302-307 GAILTT
     2   375-380 GIKGST
     3   378-383 GSTESC
     4   400-405 GNGSSV

[6] PDOC00100 PS00107 PROTEIN_KINASE_ATP
Protein kinases ATP-binding region signature

      20-43 LGKGAFSVVRRCVKKISTQEYAAK

[7] PDOC00100 PS00108 PROTEIN_KINASE_ST
Serine/Threonine protein kinases active-site signature

      132-144 IVHRDLKPENLLL

[8] PDOC00364 PS00402 BPD_TRANSP_INN_MEMBR
Binding-protein-dependent transport systems inner membrane comp. sign

      405-433 VPEGRSSRDRTAPSAGMQPQPSLCSSAMR

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	195	215	1.665	Certain
2	319	339	0.818	Putative

FIGURE 2B

BLAST Alignment to Top Hit:
>CRA|88000001156376 /altid=gi|7434378 /def=pir||JC5636
        Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123)
        II gamma-E - human /org=human /taxon=9606 /dataset=nraa
        /length=556
      Length = 556

 Score = 1083 bits (2771), Expect = 0.0
 Identities = 534/577 (92%), Positives = 539/577 (92%), Gaps = 12/577 (2%)
 Frame = +2

Query: 113 MATTATCTRFTDDYQLFEELGKGAFSVVRRCVKKTSTQEYAAKIINTKKLSARDHQKLER 292
            MATTATCTRFTDDYQLFEELGKGAFSVVRRCVKKTSTQEYAAKIINTKKLSARDHQKLER
Sbjct: 1   MATTATCTRFTDDYQLFEELGKGAFSVVRRCVKKTSTQEYAAKIINTKKLSARDHQKLER 60

Query: 293 EARICRLLKHPNIVRLHDSISEEGFHYLVFDLVTGGELFEDIVAREYYSEADASHCIHQI 472
            EARICRLLKHPNIVRLHDSISEEGFHYLVFDLVTGGELFEDIVAREYYSEADASHCIHQI
Sbjct: 61   EARICRLLKHPNIVRLHDSISEEGFHYLVFDLVTGGELFEDIVAREYYSEADASHCIHQI 120

Query: 473 LESVNHIHQHDIVHRDLKPENLLLASKCKGAAVKLADFGLAIEVQGEQQAWFGFAGTPGY 652
            LESVNHIHQHDIVHRDLKPENLLLASKCKGAAVKLADFGLAIEVQGEQQAWFGFAGTPGY
Sbjct: 121 LESVNHIHQHDIVHRDLKPENLLLASKCKGAAVKLADFGLAIEVQGEQQAWFGFAGTPGY 180

Query: 653 LSPEVLRKDPYGKPVDIWACGVILYILLVGYPPFWDEDQHKLYQQIKAGAYDFPSPEWDT 832
            LSPEVLRKDPYGKPVDIWACGVILYILLVGYPPFWDEDQHKLYQQIKAGAYDFPSPEWDT
Sbjct: 181 LSPEVLRKDPYGKPVDIWACGVILYILLVGYPPFWDEDQHKLYQQIKAGAYDFPSPEWDT 240

Query: 833 VTPEAKNLINQMLTINPAKRITADQALKHPWVCQRSTVASMMHRQETVECLRKFNARRKL 1012
            VTPEAKNLINQMLTINPAKRITADQALKHPWVCQRSTVASMMHRQETVECLRKFNARRKL
Sbjct: 241 VTPEAKNLINQMLTINPAKRITADQALKHPWVCQRSTVASMMHRQETVECLRKFNARRKL 300

Query: 1013 KGAILTIMLVSRNFSVGRQSSAPASPAASAAGLAGQAAKSLINKKSDGGVKKRKSSSSVH 1192
            KGAILTIMLVSRNFS   AAKSLINKKSDGGVK + ++ + ..
Sbjct: 301 KGAILTIMLVSRNFS--------------------AAKSLINKKSDGGVKPQSNNKNSL 339

Query: 1193 L-----------MEPQTTVVHNATDGIKGSTESCNTTTEDEDLKAAPLRTGNGSSVPEG 1336
            +   MEPQTTVVHNATDGIKGSTESCNTTTEDEDLKAAPLRTGNGSSVPEG
Sbjct: 340 VSPAQEPAPLQTAMEPQTTVVHNATDGIKGSTESCNTTTEDEDLKAAPLRTGNGSSVPEG 399

Query: 1337 RSSRDRTAPSAGMQPQPSLCSSAMRKQEIIKITEQLIEAINNGDFEAYTKICDPGLTSFE 1516
            RSSRDRTAPSAGMQPQPSLCSSAMRKQEIIKITEQLIEAINNGDFEAYTKICDPGLTSFE
Sbjct: 400 RSSRDRTAPSAGMQPQPSLCSSAMRKQEIIKITEQLIEAINNGDFEAYTKICDPGLTSFE 459

Query: 1517 PEALGNLVEGMDFHKFYFENLLSKNSKPIHTTILNPHVHVIGEDAACIAYIRLTQYIDGQ 1696
            PEALGNLVEGMDFHKFYFENLLSKNSKPIHTTILNPHVHVIGEDAACIAYIRLTQYIDGQ
Sbjct: 460 PEALGNLVEGMDFHKFYFENLLSKNSKPIHTTILNPHVHVIGEDAACIAYIRLTQYIDGQ 519

Query: 1697 GRPRTSQSEETRVWHRRDGKWLNVHYHCSGAPAAPLQ 1807
            GRPRTSQSEETRVWHRRDGKWLNVHYHCSGAPAAPLQ
Sbjct: 520 GRPRTSQSEETRVWHRRDGKWLNVHYHCSGAPAAPLQ 556 (SEQ ID NO:4)

FIGURE 2C

Hmmer search results (Pfam):

Model	Description	Score	E-value	N
PF00069	Eukaryotic protein kinase domain	309.5	4.1e-89	1
CE00022	CE00022 MAGUK_subfamily_d	295.5	3.9e-87	1
CE00359	E00359 bone_morphogenetic_protein_receptor	14.8	0.0017	1
PF00534	Glycosyl transferases group 1	3.3	9.1	1
CE00031	CE00031 VEGFR	0.3	3.2	1
CE00292	CE00292 PTK_membrane_span	-59.7	1.5e-05	1
CE00287	CE00287 PTK_Eph_orphan_receptor	-63.5	0.00035	1
CE00291	CE00291 PTK_fgf_receptor	-90.9	0.0016	1
CE00286	E00286 PTK_EGF_receptor	-131.8	0.0056	1
CE00290	CE00290 PTK_Trk_family	-154.9	0.00012	1
CE00016	CE00016 GSK_glycogen_synthase_kinase	-180.4	1.2e-06	1

Parsed for domains:

Model	Domain	seq-f	seq-t		hmm-f	hmm-t		score	E-value
PF00534	1/1	31	65	..	161	195	.]	3.3	9.1
CE00031	1/1	133	161	..	1068	1093	..	0.3	3.2
CE00359	1/1	132	186	..	272	327	..	14.8	0.0017
CE00286	1/1	14	252	..	1	263	[]	-131.8	0.0056
CE00290	1/1	15	253	..	1	282	[]	-154.9	0.00012
CE00291	1/1	14	267	..	1	285	[]	-90.9	0.0016
CE00292	1/1	14	267	..	1	288	[]	-59.7	1.5e-05
CE00287	1/1	14	270	..	1	260	[]	-63.5	0.00035
PF00069	1/1	14	272	..	1	278	[]	309.5	4.1e-89
CE00022	1/1	10	305	..	13	316	..	295.5	3.9e-87
CE00016	1/1	1	345	[.	1	433	[]	-180.4	1.2e-06

FIGURE 2D

```
   1 TTGCCCCTGG CCTGGTCTCC CTGATCAACC CGCGCCTGAA GGGTTTCTTT
  51 CTAATAATGG CCCTGGTGCT TGCGCAAGTC TAGACTGTCA GCTCCCAGAG
 101 GGAAGGCGGC TGGCAGCTGG CTCTGCGCAG GCTGGGGGCG CCTCCCGGGC
 151 GTGCAGCCTG GCACAGGCTC CTTGACCTTG GCTCTCTCCC CACGTGCTAG
 201 GAGCCCCGTT GGGGGCTCGG GACCCGCGTG TAGGACCCGT CCAGAGAGGT
 251 CAGTGGTCCA GACTCCTACA CTCCTAACAC ATGCACCCTC GCATGCACGT
 301 TCCCGAGCCC GCGCGGGGTC CGCCCCGGGA CAAGCCCATA AGTCGCGAAC
 351 CTTCCAGNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 551 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 601 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 651 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 701 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 751 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 801 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 851 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 901 NNNNNNNNNN NNNNNNNNNN NNNNNTGTAA GCCACCGGCG CCGGGCGGTC
 951 TCGACATTAA ATTTCAAAAT GTTTTCTCCG GTTTGTCACT TGTGGTTTTA
1001 CTATGTTCAA TGGGTCTCAC CAAGCAATTT TGCAAAATAG TTAACTTATT
1051 CTCTTTTTCT TACATGACTT CTTGACTTTG AGCCATAGTT AGGAAAGGTT
1101 TGCTCACTCT CACATTAGAG TAAAATTTAT CCACATTTTC ATCTAGGATT
1151 AGTGCTCATT TTTTTATTAT TATGAATATC TTCTTCATTT GGGGTTTGTT
1201 CATGTATATT CCATGAACAA TGGACGCGGG TGCAGCATTT TAGCATCAGC
1251 TATCCCCTTC CCATCCGCAA TGAGCTGGCC GCTGCAGCAG CCCCGGCCCC
1301 CCACCCCCAC CCGCGGCGCC GAGCCCGGCC ACTGCAGCCC CCGCCCCGCC
1351 CGCCCCCCCA GACGTTTCCA GAGCTCAGAG TGCCGAGCTCC CGTTTGACGG
1401 GGACGTCAAG GAAAATAGCA TGGGAAGGGG AGTTCTTGAT GTCTGACTGT
1451 GTCCTCTCTT CCCTTGCTGT CAGTTGAGCC GGGATGCAGT GAGATGAAAC
1501 CGGCTGTGGG GGGGTTTGAG CCTCACTTTG CCCCATGGTT GAGGGAGATT
1551 TCTCTTTCAG GGGATGATAC CCTCTTTTTA ATCTTTCCTT CCCCGACCTT
1601 CAGCTGTTCC TGCTGAGAGA AGGGCAGGGT CTCTCTGCTC CCTTCTGCCC
1651 TGGTTCTCTT GGCCGGGACC GCAGGGCTGT CTGAGATGCA GCAGGTGTGT
1701 GTTTTCAGCA TCGCCCACCC GCTCCTGATG TGCAGCCTGA GGTGGAGGCT
1751 GTTGCCTTGC CCAGGGACTG GATGAGGGGG TGGGAGCGCG GCACGCCACC
1801 CACATCTGTT CAGTGTCCTG CGGTGGCCGC GTCCTTTTGC CTCATGTTGG
1851 ATGGTGGTGG TCACAGCGCC GGTGTGTGTG CATGTACGTG AGTGTGACTA
1901 GAGGTCTGGT GGTGGGAGCA TCATCGTCCC CAGACTTGAA GTGTGTCTGT
1951 GTCACTCTGC CCTGCTCCGT GTCCCAGTTC TTTTCCCCTT CTCCCTCCAG
2001 GGGTGCTTTC TCTGTGGTCC GCAGGTGTGT GAAGAAAACC TCCACGCAGG
2051 AGTACGCAGC AAAAATCATC AATACCAAGA AATIGTCTGC CCGGGGTGAG
2101 TGTTCCCTGT CTTGACCTCT TCCTGAGGGT GCCTCCAGGG GCCATGGTTT
2151 CTTTTGAGGA AGCCCCAGGA ATTGGGGGTT GTGCGTTTTA GCACTTGGAG
2201 AGGAGTTGGA ATTTCAGACT GGTTGGACTT TGTGTCAGGC TGAAGCCAGA
2251 AAAGGAGTTG CATGGGGGAC TGGAAGCGCC CAGGTACAAA AGAATGAAGG
2301 AAGAGATGCA AGTAGCTGCA GTGGCCCCCA AAGGCTCAAG GGAGTTCGGT
2351 CTTCAGGGAG GTGGAGGATA TGGGGGTAGT GGGTGGTACA GAATGGGGAG
2401 CTCTTAATTT GGGGCATTTG GAGCCTCTCC CTTTGGGGCA GTGGTGGCTA
2451 CTGCAGGCCT TTCCTGGTCC CTTCTTCACC ACGGGCTGAG TTAGGATGGA
2501 AATGCAGTAA GTGAGCAGCT CTGACAAAGC CAGCCTCCCC TGCCCACCAG
2551 GCGGCAGAAC AGACTCCCAA GGGAAGGGAA TCTGTAAACA TCAGGGGAGG
2601 CTGCTACTGG CGAGGGCTTC TCAGGAACAA ATTCTGCCAG ATGAACTTGA
2651 TTGCTTTTTT GATCAAATTA CAAAGTTGGT GGTGCAGCAG CAGATGTAGT
2701 CTGTCCTGGG TGGAGGGTGA TGCCTCATGG TCTAGAAATC CCAAAGGCCC
2751 GGTTTGGGCA GGAACTGCAC TGCCTCCGAA CTGCACTGCG TCCGAGTCTG
2801 AGGAGCATAA AGGCCAAGGC CTTGGGGCCT CACTTGCGAG ATCCTCCCAA
2851 GTACCTGAGG CTTGGAGGGT CAGGGCCTGT CTTTCACACC TTGAACCTAC
2901 ACTCTCTGAA CTTCCTATTG GGTACTTGCC AAACTCACCT CATCTGATAG
2951 GTGTAGACCC AGCAATGTGT GAAGTGCTCT GGGAACAGGT CTGGTGAGTA
3001 CAGAGGTCAG ATCTCGGAGG GCTGCAGGGT GCAGCTGGGG GACAAAGGTT
```

FIGURE 3A

```
3051 GTGAAACTCA GAGAAAGGAA TTAGGGCTGG GCAGTAGGAT GCCATAAATA
3101 TATTTGGAGC CAGGACACAT GCCCTGGGGA AGACATGGGC TTTGGCCAAT
3151 AATGACACGG GTTTCTCTGG GATAAGAGAC ATAATAGATG TCCCAAATGC
3201 TTAGAGAAGC TCTACAATTC CACGGGCTTC TGTCGTGTTG GCAGTTGTTC
3251 TGGGACCTGT TTAGCAGGGC CGTGTCCACT CCCTGACTGG GGACTCTCTC
3301 TCCATCCCTC TGGTAGGGCA CTAATTGCTG ACTCCCATCC AGCTCCATCT
3351 CTTGCTGTTC GTGTACATTG CCTATAAAGT TGGACTTGTT TGTTTTCTTT
3401 CTCTCTGGGT ACCTTGAGTC TGAGGATGGT TGCCATAGAG ATATGTGGGC
3451 AGTCAGATAC CCTGGAGTGG GGGTGGGGGG GACAACAGGG GCTGGGCTCT
3501 CTGGCAGACA TCCTCTGGCC AAGGATGGAA GGTGCAGGCA GGAACAATGG
3551 CTTGAGGCTG GATACCTCTC TTGCCCACAC AGCAGAGCCC TGGTGCATCA
3601 GAAACAGGGC TGGCATCTGG TGTCTCCAGT TGATGATGCA ATGCTTTGCT
3651 CTCTTCATCT CACCAGTGTC CTCTGACCCA TGGGTAAGAG AAGGAGAGAT
3701 GGCTGGGAGC CGAATTCTGG GATGTGAGGA TAGGTGATGT GGTGACTTCC
3751 TGCAGCTGCC TGACTGGGGC TTTCATTTCC TACTCCTTCC CTACCTGCGT
3801 AAATTTCCAT GACCTGTGTG ATAGCCTCCC TTTCCCTTCC TCACCTCCTT
3851 TTAACCTTGT CCCATCTTTC CCAATGGATA TCTTTCCCTG GCCAAACTGG
3901 ATGAGACTTG ATTTCTCGTT GATTTTTTTT TTTTTCCCCT CAAGAAGAGG
3951 ATTCTTGTGT AAAAGTATAT GCTTCAGACA GCAACTCCCC CTCTCCCAAG
4001 ATGGATATGC CAAGACTGGG CTCTGTTGTG TGGCCTCATG TGCCAGGTTG
4051 ACTTTGGGAC AGAGGCACAG ATGATAGGCA CAGATGCCAG CCAGAGGGGT
4101 CAGAATGTGT AAGTGCCAGC CAGTACTGTG TGGAGGTGGG AAAGTGGAAA
4151 GGGGCTGTCT TGGAGATGGA GGGAACAAGG TGGGGCTGGA CTATAGGTGT
4201 GGGCATGGGA GATGTGAACT CCTGGAGAGA TCTGGGCCAG GGTAGCCATG
4251 GGCTGGTTCC CATGGGGTTA GGGAGTGAGG GCCATGGCTT CCCTGCAGAC
4301 TCTCAGTTTA CACTATATAT TTTATAAAGG TGCAGCCACT GGAGCTGGGT
4351 TTCACTCATC GCTGTCTGCC TAGGTCTCCG CAGGTGTTGG ATTTCTGTGT
4401 CTGGGAATGT CGTGGGCCCA CCAGGGTCAT CTGTGAAGGT CTGAAGGGGC
4451 TTGCTGTGTT CACTGGGTCT TCCTGCCTCC TGTCTTTCTT GTTTGTGATT
4501 CTCTGGGCTA CAAACTGAAA AGATAAAAAG AGGGTATAGA GCTGTTTCTC
4551 CTTGGCATCC CTGGTGAGGT GGCTAGGAGT CAGGGAGAGG GATCACCTGT
4601 TCTTCTGGGG GGGTCCAATC GAGACAGGAA GCCTTCTTTT GGGCTGTTGT
4651 GTCTTGTCAC TGTGGCCTCA GAGGCCCACA TTGGCGGCTA GGTTGCAAGG
4701 TGGGGAGTTC ATGCGGATAT GCGTTGAGCA CTGTCTTTGT CTGCGGGCCT
4751 GTCTACATAA AGTCACTGAA AGTCACATAA CGTCACTCCG TTTGCTTCAG
4801 AACCGTGATA GGAGTGGAGC TGGGCTCTTA AGGGAGCCCA TGGTTCCAAG
4851 CTTAGCTCCA CTAGGCCGAA GGAGGCATTT AAAATAGGCT TGGATGCAGG
4901 AGCTAGTGGG CCAGGTGATG GCAATGATAA GTCGTTATTT TAAGATTTAA
4951 GAGCACCCCC CTCAAGGAGC CTGAGCCCTT ATGTCTTTTT TTATTTTTAA
5001 ATCTTCATAT TCCCTTCTTA TCTTTATTCA TATGCATACA GATTTTCACC
5051 TCGTGGAGCA TAACATTTTA TATCCTGCTC TCTTTGCTTA TATCCAAAGC
5101 ATTTCCCCCA TATTACTACA GTTGAAGGGC AAATGGTCCT TTCTTCTACG
5151 TCGTTTAGGA TTTATCCCTA AAACAATCAG CATCACAAGA AACTTCTGTA
5201 TATGTACCAT TTATCTGGAT TCCAGTTGCT TTTACCAAGA TAGATACTGG
5251 GGTAATGCCC TTGGCCTTAC TAAGAGATGC TACCGGAAAC AGTGTTTTGA
5301 AATCTGTTAT AATACTTTAA CATATTTATT TAATCTGTAC ATTCCGTGTG
5351 AAGAAATTTC TTTTGAAGCT AAATGTAAGC AAAAGCTTTC CTCTTTGTGA
5401 GGACCTGAGA GGTGAGGGAA GGGTCCTTAT GTGTTTCTAT ACTTCTGCAT
5451 GGGCAGGCCC TAGCGAAGTG CCTGACGTAT GCCAGCCACA TACACATTAA
5501 ATGAATGGGT CAAGAGGACT ATGTAACCAA TCATGGTTGC CTTTTGGCTT
5551 TGGCTCCTAG GAAACTCAGA GTCAAGTTGC CAGAGCCCTT GTACCCTGCT
5601 ACAGACTTGG GTCCTCCCTT TCTGATCCAG GGAGCCAAGC TGCAGACCTG
5651 ATACGGCTGC TGGAAGAGAG GACAGATGAG GATAAAGACC TGTTGCTTGGG
5701 GCATAAGGCA GAGTGGGAGA TGTAGGCAGA CATTTAGCTG ATGATTCCTC
5751 CTTCCCTGTC ACTAAATGGC ACTATAGGGC CACTGTTGGG ATCTCTTCCA
5801 GGTAGTGATT TTCAATTTTA GTGTGCGTAA GGATCACCCT GAGTACTAGT
5851 TTAAAAAATA CAGACTTCTG GGCTTTAGCC ACAGAGATTC TGCTTTAGGA
5901 GGTCTAGGGT GGAGCTGCAG AATCTGCATT TTTAACACAT GCTCCAGTGA
5951 ATTTCATGCA GGTGAGGCAT GAGCCCACTCT TTAAGAGATG CCACCTAAAA
6001 TCTGCAACAA CAGTTGCTCT TGCCATGCCC TCTGGAATTC AACAGACACA
6051 CCTTGGCCCA TCCTTCTCCA GATTGTGTGT CTGCCACTAT GTGGCCATCT
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FIGURE 3B

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6101 GTGCACATGG GCTGTTCTGT GATTAGGGGC CTCGTTCTGG GCCTCGGGAT
6151 TGGGGTGTCT GTGTCTGAGG CTGCGGCAAG CTGGGTGGCT CGGGTTGTGG
6201 CATGTTGGCC ACCAGAAGGG TAAAGGCTGT CCCTTTCTGG GTCCAGCTGG
6251 CCCTGGGGAC TGAAATGGGA TCCCCTGGAT GGTGCCAGCT GAGAGTCCCC
6301 GCCCCCTTAG TGTTGGCCTG AGTAGCCCCC ATGACATTTG TGTCCCCTGT
6351 GGTATCTCCA AGTGAGACTT TCCTGTTAAG GATCTGGGTG AAGTGAGGGA
6401 AAGAGAAGGG AGGGGGAAGC AGTAATGCAG GGAGTGGGAG AAGGAAGAGA
6451 AATCCACACA GCACTGGAAC ACAGGCCTCG AGGAAGCATT TAAGGAGGCT
6501 GTGTGCCGAAA CCATGCTTTC CTCCTGAGGA TAAAACAGGC CAATTTCTGT
6551 AAACAGAGAA ATGGGCATCC TGCATATCAG TGATGGAGCG CCTCTACTTT
6601 CTCTCCTGAA GGGATGGAAG CCGACTGCAG GTCCCTCTGT GCAAAGGCTT
6651 CTGCCAGGCG GCTTTTGTCA CGCGGTCACG TTGAGCTGTG GGCCTTAGCA
6701 CACACAACAC TGGCCTGTCC CCCTCCCCTC CCACCTGTCT TCCTAGAGTG
6751 ACTTGGGGTG CTGCATCATG GTGTGGGGAT GGAGGTGGGA AGGTTGCCCT
6801 GTCCTGTCAG GGAGGCCCCT GCCTTCTTCC TGCTGCTTCC TCTGGTCCCT
6851 TGTCACCATA CCCTTGTTCG AAGCTGTGCT GAAACCCTAG AGGTGAGTGG
6901 CTGACCCCAT TCTCTGCTGA GACTGGGAGAT AGGGAAGGGG AGGCTGGGTG
6951 TGACCATTCC TGCTCCCATC TGTATGCTTG CTGCTCTCTG AACAGCTTTG
7001 GCAGACCAAC AAGGGCCTGA TCCCATGGGT GCCAAAAGGG TGGTGACAGG
7051 AGGAGATGGG CACTTTGCAC CTCTTGAATG CCTCTCTGCA GAGCCCCTTT
7101 GTCACCTACC CATGGCCAGA CAGATCTGCC GCAGGACCGC TGGGGAAATC
7151 AAAGCACAAA AGCTTTGTCT GGGGTCTTTT TTTTCTTTTT TGGTTTTGTG
7201 CTGCAGGTGC CCATGACTTT GCCAGGGCTC AGACCCAGCG TCCTCAGGCC
7251 GTGTGGCCTC CACCCACTCC TTGGCGCCTT TCTTTAAAAC ACAGGTTCTG
7301 GATACTTTGT TCCTGTGATG AATCTTGGCA TATCACCTCA CACCTCTCCA
7351 TCTAGGCCCC AAGCTCCAAG CCTGGTGGAG CAAATCCCTC CTCGTTGCTG
7401 GCTGAGGCCC CATTCCCGTC TGTACCCACC TCTCTGGGCT GTGCGGTGGG
7451 GAGATTTCCA GCCACTCCTC CCCAACACCA TCTCCGCTTC CTGGGCCCTA
7501 TCAGCAGCAG CCGCAGCTTC CCATCTGCTC CCCTCTTTTC TCCTCCCTTT
7551 CTTTCCCTTC CCCCCTGCTT GCTGCTGCCC TGGGAGGAGC TATTTTTAGG
7601 GGCTGCTTCC TGGGATGTTT TACTTGGGGC TGGTTACCAT GAAGGAAATG
7651 TCACCAAAAC AGTGGGCAAA GGCTGCAGGC ACCGGGAGCC CTGCCGGGGG
7701 GCATGGAGAA CAGACGGCTG ACCCTTTTCT GGCCCTTGAG AGCAGCCAGA
7751 GTGCCCCCAG GCAGAGCCTT GCCTTCTTGG GGCTTGCTAG TGACCCCTTG
7801 GGGATTTTCT CTGTCAAAGC TGATTGAGGG CCTTTTCGCT ATAGGGCATT
7851 TCTTGGAGCC TCTCGCTTCC CTTGCCTTGA GATCCAGAGG CCAAAGTGGG
7901 GCTCAGGTCT TTGTGTCACC AAGTTAAAAC TGCTTGAGTG AGGGTTGAAG
7951 ATAAGGGGAG GATGCTGGGT ACATGCACAG AGCCTTGGGG GTTCACATGG
8001 GACCATTTCA GGCCCCGTCC CTCTGTATCA CAGCCCCCAG CTAGTCACCA
8051 GGTGTACATG TGTGAGGGCA TTAGAAACCA TGGTCCTGCT CTTGTGTGTC
8101 GGATGGACTT TGCTTTTAAT TGGAGACTCT TTGCATCTTT AGAGTGAGAT
8151 TCAAAGAGGA AGGGATGTGG CATCACAGTG TCAGGGTGAG GTCGGTGGGA
8201 TCGTGGCTTG GGATTCCCAC TGGTCAGTGT CCCAGGCCCA GGGCTGTGCA
8251 TAAGCAGCTG GGGAAGGTGG ATTATGACAT CAAATCCCTG CGATGTCCTT
8301 GTTTCTGCTC CTCAGAGTGC CAAGGGGACC AGACGGCGGC CTCTGCTGCT
8351 TGGGAAGAAG ATGAAAGGCA CTCAGGAGGG CAGCAAGTGA GGCCGCCTCC
8401 CATGGAGCCC TGAAATCAGT GGGGTTGCAG GAAGTTTCTC ACATCCATGT
8451 TTAGGGTCAT AGGCACAGAC CTGCAAAATA CCCTTTGCAA AGTTAAGAAT
8501 GTCTTTGAGA TTGGAACTTG GGAGAGTCCT CAGTCAGAGT AGGAATGTGC
8551 ATCCTTTCCC ACGTACAGAG GATTGTATGT TTACGTGGCA GCAGGATCTT
8601 ATTTGAAGCT AGTGCTGGCA TTTGTGTTTT TTTTTTAGGA AAATGTCACT
8651 AAGTCAAGCA GGCCCATCCC TGAGAGGGCC ATGGAGAATC TGTGGCCAGC
8701 CCTCCCTGGC CCCCTGACCT GGCAGAGGAA GGAAAGGGCA TTGGAGTAGG
8751 CTTCTGTCTT CAGGCCAGAG GGGGAGGTGG TTCAGGGGCA GGCTTGGTGC
8801 ACCCCTTGGC TGCAAGCTAT CACCTCCCTA TCTGCTTCCT CTTTTCTGCC
8851 TCCCCTGGTG CATCTGGTCA CTTCTTGCTG CCCTTCCTGT GAAATCGTGG
8901 CACCTTGGAC CAAGTCCTGA AGCACTTGGG CAGAAGGCGG GAGAGGTTGG
8951 GTTTCTAGGA TCCTTGTTTC CCAGGGCCTG GCTCTGGCCT GGGCTCAGAC
9001 CACTCTGGTC TAGGCAGGCT GCTGGGGAAA GGCTGGAGCT GCTTCTGCTT
9051 TCTGCTCCTG TTGCCACCTC TGCTAATGAT GGGGAAAACC TGCAGAGGGC
9101 TGTGGTTGGA GCTGGGCTGA AGGCCGGCAG GGGTGGGTCT CTCCATGGCA
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FIGURE 3C

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 9151 GTAGCACACA GGCAGGCAGG AAGTGGCCCT GTGCAAAAGC GGGAAGTGGC
 9201 AGTTGTCAAA CAGGAAGGGG GGGGCTGGGC TGTGGGAGGG GCGGGGATGA
 9251 GCCTGGGTAGA AAGGTGCGTG GAGGAGGGTC CACCTTGGAA GGTCTGAGCC
 9301 TCTCCCTAGT GGTTACTGGA AGGAGGGGTG TCTCAAGGGG AGACACCTTT
 9351 GCAGCACCTT GAGATGCCGA GCCAGGGCCC TCCCACTGTG GACCAAGCCC
 9401 ATTCAGTGGC CTCGCCCTTT TTGGGGTTGG AGATGCTGCG TCCAGCTGGG
 9451 ATGCCCTTGC TTTTGGGAAA GATGCTCTAG AAACCACTAC TCCATCCTGG
 9501 AACCCCTCTG CTGCCACTGC TGCTGGGATG GACCCTCTGC TTTTTTGCAG
 9551 CCGTGGGCCA GCCCTGGATG TGACTACAGG ACAGGAAGTG TCAGGGGAAG
 9601 AGACAGGAGA CAACAGCTGG AGAGGCTGGG TGGTGGCCGG GCAGTATGTG
 9651 GCAGCAGGAA CGGGGAGAGC GGGGCAGGTA GAAACTGCTC TGTTCATTGA
 9701 GGAGAGCTTG TGGATGGCAG GGTGCCACGG CTGCGAGGAA GAGGAGGGAA
 9751 GCGGACAGTG GCACTTCCTG CGGCGTTCCC CTCTCTCTGA GGAGCCCCTG
 9801 TTGCTGCCCA TCACCTGCAG ACTGTAGACA CAGGTGGGCC CCGCCAAAAC
 9851 AGGGAGGGAC ACTCCACCTC CAGGACTGCA ATGGAGGACC ATGTGGGGAG
 9901 CCCAGAAGCC AGGCAGGAGG GCTTAGTTGC TGTGTTGCAG ACCCTGCATC
 9951 TGCCTGGGCT GAGGGGACAG TGGGTCCCAT TCACAGTGTC TCTGGTGATA
10001 GCTGTGGCCA CAAGCCCAGC CCAGGAGACC CTGTCAAGCT TCTCACTGGG
10051 CCCTTGGAAA GGAGCTATAT GCCAGACCTT ATGCAAAACT CTTGACCTGT
10101 ACCACCTCAG TTAAACCTCA GATCTTGCTG TCTCTATTTT AGAAGTGAGG
10151 AACCTCTTGG CCGGGTGCCG TGGCTCACGC CTGTAATCCC AGCACTTTGG
10201 GAGGCCGAGG CAGGAGGATC ATAAGGTCAG GAGATCGAGA CCATCCTGGC
10251 TAACACAGTG AAACCCCGTC TCTACTGAAA AATACAAAAA AATTAGCCGG
10301 GCATGGTGAT GGGCGCCTGC AGTCCCAGCT ACTCGGGAGG CTGAGGCAGG
10351 AGAAGGGCGT GAACCTGGGA GGCGGAGCTT GCAGTGAGCC GAGATCATGC
10401 CACTGCACTC CAGCCTGGGC AACAGAGTAA GACTCCATCT CAAAAAAAAG
10451 CAAAAAAAAC AAACAAAAGA AGTGAGGAAC CTCTTTCCCA AGATAATGTG
10501 CCTGGCTCAC TGTCTCACCT ACTTTGGGTC CTAATCAAAT GTCACCTCCT
10551 TACTGAGGCT TTCTTGGACT GCCCTACTCA AATCTGCACT CCCCACTTTC
10601 TCTGCTTTTT CTACGCAGCA CTTGCCGTGA CATCTAACGT GCTGTTGAGT
10651 TTTCTTACTG TCCATCCCTC CCCCATACAC AACCCACTAG AGTGTCAGCT
10701 CCATGAGGGC AGGGATTTTT GTCTGTTTTG TTCGCCACTG TCTTCCTAGC
10751 ATCTTGAATA CTGTCTGTCA CATAGTAGGC CTCAGTAAAT ATTTCTTTTT
10801 TTTTTTTGAC TTGCTCTGTC ACCCCAAGCT GGAGTGTAGT GGCCCAATCT
10851 TGGCTCACTG CAGCCTCCAC CTCCTGGGTT CTAGTGAGCA CATTGGCTA
10901 AATTTTGTAT TTTTAGTAGA GATGGGGTTT TGCCATGTTG GCCAGGCTGG
10951 TCTTGAACTC CTGACCTCAA GTGATCCACC CACCTTGGCC TCCCAAAGTA
11001 CTGGACTGGG ATTACAGGCG TGACCCACCG CGCCCAGCCA CGATAAATAT
11051 TTCTTGAAGG AATGAATGAA GCTCGGGTGG GTTTAATAGC TTGCTGGATG
11101 TGGCAGTGTT GGGCTCAATC CAGGGCTGTC TGACTTCAAA ACCGATGTGT
11151 TGTTAATTGC CATACTCCAC AGCTTAGAAT CAGAATGAGG ATCAAGGTAT
11201 AGTCCTGGGG TTCAGAGAAG ACCTGGGCCT TGCCGGGAAC ACAGGGCTCA
11251 GCTCCTTGGA GTTAAGGCTG AACTAAGAGG CTAACAAGGA CCCTCTGGAT
11301 GCTGGGCAGC TCCTTTGAGG AGCTGGGAGC CTGAGTCTGT GTATCTTCTC
11351 TCCACTCAAA GTCACTGGTA AAGCAGAGTG CCCTTATTTT TAGTGCTGTT
11401 GCTGTTGTGG GACTGTAACC ATTAGCTAGT AAGAGACTTA AGGAAGGAGA
11451 TAAACATTAA TCTTCTGGGC CTTCCCTCAG CTGCCACCTC CGCATTGCAA
11501 GATGCTGTTC TCCTGCACCT GCCCAGGCAA CCAAGCCTGA GAGTTATGGG
11551 CTGGAGGGTG GTGAGGTTTG TGCCCAGAGA GAGGGCCGTG GGTCTGTAGC
11601 TTTGGGGCTG GCTGGCTTGG TACCTCCATC TCAAGTCCAG GGATGGAAGG
11651 AAGGTGGGGT CATGTCAACA TCCTGCCAGA TCTGGAAGAA GCAAGCCCCC
11701 CAGCCACCAG GCAAGGCTGT TACAGCCTCC TTGAGTGCCT CGCTTCTGGA
11751 GGTCACTGGC CACATCCCTG TGCCTGGGAC CAAGGGATGC CAGGTGATCT
11801 GGGAGTTGGG AGTTACTTGG GGTTCTCCTG GCTGCATCCT GGTCGGTGGT
11851 CATGCTGAAC CCAGGCACAG GAAGGAAGGC CTGACCCAGA TCTTTGGGCA
11901 GCTGGGACGG ATTAGCTGGG CAGCAGGAAC TAATCTCTGT CTGTCCCCAC
11951 CTCTTTCCAC AAAGTAGAGC TGTTGCTAGA GGGAAAGTTT AGGACAAAGC
12001 TGGGTTTGGT TAGTGAAACA ATAAATGTGA ATTCTTCTA GTCCATAAATC
12051 CCTACATTAT CTCACACTGA CAGTCCTGAG TTTGAATCCC CCTTTTATCC
12101 CTTTCCTGCT GTGGGATCTT GGGCAAGTTA CTTAACTTCC CTGGGCCTCC
12151 GTTTCTTCCA TCATCTGGAA ATGTGGACAA TCATAGCATT TACCTAATGG
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FIGURE 3D

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12201 GATCATTGTG AGGGCTGTGG GAAGATTTAC AGAAGCTTTT TGCTGTTTAG
12251 GGTAGAGGCA GGGAGACAGG AAATAGCTTGG CAGCTATGGA TGTGAAGGCC
12301 CCTGCCCGGG CCTGGATAAT TCAGGGTGAA CTGGACTCTC TTCCTTTTGC
12351 ACCCCCTCCA AAGCCTAGAG TCTTAACTCA ACTCTCACCA TTCTTTATCT
12401 GGCCATAATA GCACAGGGGT GGAGAAAGAG GGCTCTAGGC TCAGACCACC
12451 TGCATCACTG CCTGTTCGTG TTACCTTAGG CAGATTACTC TATCTTTTTA
12501 AACCTGTTTC CTCGGTAATA TAATAGAGCT AATCAGATCC CTACTTCACA
12551 GAGTTTCTGT AGGTATGAAA TATGGTAATC CATGCCTCTG CCTGACATGT
12601 AGTCAGTGCA TAGTAAGCGA TTGTTATGGC GACTACTGTT ATTAGTAAAC
12651 CCTTATTAAG CCCCTGTTTA CAGAAAGAAC TCTAGAAAGC ACTACCTGGA
12701 AAGGTACCCC CGCCTTCGAA GAGCTTGCAA CTGAAAGATA ACTGATGTAA
12751 TATATGATGT GAGAATCGTG AGAAGTGCAT TGGGAAATCG GGGGGGGGGG
12801 GGTGGAGTAG GAGGGAGAAG TCACAGTCTA CCGAGAGGAG CAGGGAAGAC
12851 TTCATGAAGG AGGTGACTTT TGGCAGGATT TCAGCAAGTA GAAAGAGCGA
12901 AGGACAGTGG GGGAGGGCTG TGAGGCCTCC GTGCTGTGAG TAGCATCCTC
12951 TCTTCCCACG TACTGGAGCT CTGCCTTCCT GTGGAAGGAA TTGACCCACG
13001 CAGCTCACTT GGATCTGGGG ACTGTGTGGAT TTCTGGTTAT TCCACCAAAA
13051 CCAAGTAATC CTGGAGTCTG AATTTGAAGA GGTCAAAGCT TACAGCCATG
13101 GTGGCCAAGA GGACTCCGGG GAGAAGCAGG ATTTGTGTCC TGGTTTCTCT
13151 TTCTATAAAA TGGGCATCAT ACTAATGCCA CCTCCTAGAT TGTTATGAGG
13201 ATAAATTAAA AGAGGCAGCT GCCTGGTGTA GAAGTAAGCT CTCAATAAAT
13251 GTTAGCTATT ATTATTTTAA GTCATCATTA TCTTGATCAT CAACCTCTTT
13301 ATTATCAGCA TCATTATGTT TCAGGCTTGC CATCAGGACT ATGTAGAGAA
13351 TATATGCAAA ACCCCTAGCC AGTGCCGAGT ATATATTAGG TGCTCAGTAT
13401 AACTTAGCTA TTATTAGTGT TCCTAACAAG AAAGAGATTC TGGGCCAGGC
13451 GCGGTGGCTC ACGCCTATAA TCCCAGCATT TTGGGAGGCC GAGGCGGGTG
13501 GATCACCTGA GGTCAGGAGT TCGAGACCAA CCTGGCCAAC GTGGTGAAAC
13551 CCCGTCTCTA CTAAAAATAC AAAAATTAGC CAGGCGTGGT GGTGTGTGCC
13601 TGTAATCCCA GCTACTCGGG AGGCTGAGGC AGGAGAATTG CTTGAACCCA
13651 GGAGGCGAAG GTTGCAGTGA GCTGAGATCA CACCACTGCA CCCCAGCCTG
13701 GGCAACAGAA CGAGACTCCG TCTCAGAAAG AAAAAAAGAG ATTCTGGACA
13751 CCCTGGACCA CTGAAACCCT GTTGTGGTGG AAAGAGCACC AGAGTTTTAG
13801 TTGAATACCT GGATTCAAAT CCCAGCTCTG CTGCTCACTG GCTCGAAGTG
13851 TGCAAACCCT CAAGTCATTT CCTCATCTGG AAAAGGTGGT CATAACTATC
13901 TATCTGGCCC AGGCCTGGTG GCTGGTGCCT ATAGTTCCAG CTATTCAGGA
13951 GGCTGAGGTG GGAGGATTGC TTGAGCCCAG GAGTTTGAGG CTGCGATCAT
14001 GCCACTGCAC TCCTGCCTGA GGGACAAAGT GAGACCCTAA AATGAAAGGA
14051 AAACAAGTTG TCTCCAGGAT TGCCATGACT TGCTGCATTA CTTCAGCAGA
14101 TCATCACAAA TGCATAGTTA GTACCTGAAC TGAAGGAATA TGAATAACAA
14151 GGTGACCACA AGGAGAATCG ATGGTTGATG GCTTTTGTTT TTTCTCTTCT
14201 GCTTTTAGAT CACCAGAAAC TAGAACGTGA GGCTCGGATA TGTCGACTTC
14251 TGAAACATCC AAACATCGGT GAGTGCCTGG GCATGGAGCA TTTTGTGGGT
14301 ATTTTGTAGA AGCAGGGATA ACAGATATCC ACTGCTTTTG TGTGTGGGAT
14351 CACCTCTGTC TGTGGACCTT CACCTGGTGT CTGTTTTTAC ATGAGCAGGA
14401 TAGCAACTGT GTCTCAGAAT TCTGGGGCAT TCTAGTTTAG AGACCTGAGT
14451 ATCTGCATCA CTGCGGCACC TTCTCAGGGC TGGGGTGTGA GGCATCAGAA
14501 TAGGTTTCAG ATGCTATTTC TTCCCTTTCT CCTTCTGTCT TTGGGCTGAG
14551 GTCCAGGGTC CTCAGCGTGT GAGGTTCCGG GCTCCTAGCC TGCCAGCGTC
14601 CCTCACCAGG GGCCATCCAC AGCCCTCATG CAAGGGTCAG GATTTTGTTT
14651 GTGGACCTGA AAGAGTTTTG TTCCTGCTGC GGTGTCCTGC ACACTCTGGG
14701 GGTTTCCATG GTGCTCCCAT TTGTATTCCC CAGAGCCAGG AAAGCAAGCT
14751 GCCCCCCTGC CTGGCTCCTC TGGCAGAAGG GATGGCAGGA ACCACTCAGT
14801 ATGGGGAAGG AGAAAAAAGA GGATTTCTCC CTGCTCCCAC CCTGACTGGG
14851 GGGACAAGAG CACATTGTTG GTTGTGCTAA AGCCTGAGGA GGTTTGCCTG
14901 CCTCAACCCA CTCTGGCTCA GTTTTACTTT GTTCAGCTGA AATGGTCTTT
14951 GCCAAAAGCG TTGGCCCTGA TTTGGTGCTC CTTGCAGAAG GGACAGAAAC
15001 TGGGCTGGCT GCAGTGTCTG AGCAGAAGCC CCAGTGTTGA CTTGAGGCAG
15051 AGCAAGGAGC ATCTCCTAGG TTTTCCCTGA AAGCCCTGAG TCATCACAAA
15101 AGACAACACG TGTTCTGTGC TCCTCAGGCA TGGCCTAAAT CTCAGGGCTC
15151 CCACCGTGCC CCAGAGGTCG CCTGCTCTGC TCTGTTGGCG GCCAGGGCTG
15201 TGAGGTGACT TGCTGAAGCC TAATGCTTCC TTCAGAGCTA CCCAGCCCCT
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FIGURE 3E

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15251 GGCTTCCCAG GTCTCGGGCT AGAACAGTCA AAGTGAGCTC TGTCATGGAA
15301 GGGCTGAGGT CCTGCTCTAG CCCTCTGGGA GAGGAGCAGC TCTGAGGTAG
15351 TCAGAACGTC AGCTGTGCAG GGCTTTCTAG ATGGCAATCA GCAGCTTGGA
15401 TTACACCCGA AGCAGATTGG TGTGGCCAGT GGTGATCGGC TTTGCCTGAT
15451 GCAGTGTGTT CTGCAGAGCC AGCACCTCTC AGCTGGTGGG TTCCTGGCCG
15501 CAGAACTACT GGAGCTCCTA GGTGGTTTCT GAGGTTAGGC CTTCACCTGA
15551 AAACAGCGCA GTGGGGACTG ACATGTTGCC TTTGGTAGGA GAGGGCCCAC
15601 AGAGGGAAAC ACCTAGAACA GCAGTCACAG ATTAGGCATG TTTTGCTTGG
15651 CTGACTCAGT GGTCTAAAAA TATTTTTATT ATTTGCCAAT ATTTAAAAAT
15701 GAGATTTCAC ATTTTGAAAA AAGAAAAAAT CTATTCCCCC GCCTTTCCAG
15751 TCAGAAGGCT TGGCTCTGCT GAGCCCCCAC CTTGCATGGC CAGAAGGAGC
15801 TGTGAGGAGC GGTGGCTGCC CCTGCAGCCC GCTGGCCACT GTCCTTGTCA
15851 CCCACTATGA GCTCACATTT GCATTACCCA CCTGGGCCCC TGTAGGCCTT
15901 GCAAGCTTGT GACCTCTAAC CTAGAAGTTC CAGAACAGGA AGAAAAAACA
15951 TGTGCGTGAC TAAAGCCACC CATAAGCACA GAAGCATTTT GATGTTCCAG
16001 ACCCGGGTCT CAATATCTGA GGAGGGTAAC TTCCTTTCCT TTATGCTCCT
16051 TGTGACCAAC TGGTACAGCA GTGATAATTT GTCCTCATGT AGGCAGGAGA
16101 ACAGCAGCTA GGGGTCAGTG ATGCAGGAAG CAGAACCATG TCCACATCAC
16151 CCGCGATGCG GGCGGGTTGA CCATGGGCGG GTTGACCACG GATGGGTTGG
16201 CCACGGACGG GTCAGGGTAT AATGAAGACA ATTGAGAAAT GAGCAGGAAG
16251 GACAAAAATA GAATTCTAGG TGAAAAAAGC CCTAGGTGTC TTTTTATTTA
16301 TTTCTAGAAT TAAATACATA CTTTTTTACC CCATAGACTT CACTCTGTTT
16351 GGTAGCCCTT TACTTTTACC ATCTGCCCTC GGCTCAGAAT GGAGGCAGGC
16401 GGAGGGACCA TATATCCTGG CCGTCTGCTC AGAGGCCAGG TGGGGCACAG
16451 TCACTCTTTT GGCCTCTGAT TTCCTAGAAC TGTGCTTCCA TTTCATGACT
16501 GCTCCCAGGT CCTAAGGAGG TTGGTCCGAG GACCGGATTCT GGGGTTGAGG
16551 GTGGGCAGAG GGAAGGGGGA GTCAAGACTG TGTCCTGGGA GCTCCAGCAT
16601 CCGGTGGGAA CCAGGGCTGT TGGAGATGTG GCGGAGCTGC AGGTCCAGGC
16651 GGCTGTGGTT GCCATGGATC TGGACCTGGC TTGTGGCAGG AGAGGAGGCA
16701 ATTTTGTGCC CCTAATTCAC TATTCCTCTT CTCTCTCCAC TGCGCTGTCC
16751 TTCAGAACTG TGACCCTTTT GGCTCTGGCC TCTTGAACTC CATCCCAAAG
16801 GGAAACAAAC GGGCCAGCCC AAGAACAGTG CACAGTCGAG GAAGCTAGAG
16851 CAAAGAGCAT GTGGTCAGCC CTGCCTGTGG TCAGACTCGG AGGCACTGAA
16901 TTCAGATGGA GCATTGGTG CTAGGGGCCA GTCATGCCCA GTTTCCCCTT
16951 AATAGCTAGT ATATTCTGTC CCAGGAGTTA AAAGCCTGTT GGAAGAGTGA
17001 ACCCTGATAT AAACTCTGGA CTTTGGGTAA TGATGATGAG TCAATGTGGG
17051 TTCATAGACG GTAACAAATC CACCACTCTA GTGGGAGATG TTGATGGTGG
17101 AGGAGACTGT GCATGTGGGG GACGTGGGGT ATTTGGGAAT GTTCTCGGGT
17151 ATTTGGGAAC ACCCTGTACT TTCCGCTCAA TTTTGGTGTG AACCTAAAAC
17201 TGCTCTGAAA ATAAAGTTTA TTAATTAAAA ACAAACAAAC AAACAACAAA
17251 ATGCCTGTTT GGGTGTAAGG CACACTGCCG AACTCCAAAC AGCGCTGGGA
17301 GTGTGGCCAG TGGTGGGGAG TTGAGAGGAG GAGACGCTGG TGTGAGGTCT
17351 GAGGTCTGAA TGAAGTCCGT TCTACCTGTG ATCTGCCTGC TCCCTGCTCT
17401 CAAGTCCTCT AATGAATAGA CTCTGTCTTC CTTCGTGCTG AGCTGCCCCA
17451 GCAGTTTCGA TCATAGTCTA GCATTGTGGT TTAGAGCAGC ACTTCTCAAA
17501 CTTTTATGTG CTTAAGCACTC ACGCAGGGAT CATGTTAAAA TTCAGATTCT
17551 GATTCAGGGG GTCTGGGGTA GGACCTGAGT CTCCAGCTGA TGCTCATGCT
17601 ACTGGTCCGC ATGCCTGTCA ATACTTGGAG AAGCCAAGTT TTGCCGGCTTC
17651 GGAGTCGCAT CCAGATTTGG GGTTTGAATC TGGGATTTGC TAATTAGTAA
17701 CTGTGACCTC TGGCAAGTTA TTTAACTCCT CTATGCCTGC CTCTGTTTTG
17751 TTATCTGGGT CCCTTCGTGG AGTTGTTATG AAAGGGTTCA GCCAGGAAAG
17801 GGGGCTAGGA GGGAGATGAT GAAAATGGAG ATTCCAGCCC CTAGAAGTGA
17851 TCTCTTCAAG ACCCCCAGCC TCGACTCAGT TCACAAGTTA TTCAAGCCTG
17901 ACCATTTACC CTTGAGCCCA GTACCCATTC AGCTAACAGT AAGTGTAGCA
17951 AAGAAACGGT TGCAAATAAA AAGAAACATT GAATCATGAC TGAGCAGTTC
18001 CTACATCCCT GCCCCCATGG TGGGGGTGGG GGGAGCCCTG CCACAGTAAG
18051 CTCTTGGGGG GCAGCTCAGT CCCCCACAAG CCCCCATGGC AACAGGACCT
18101 CCTTCCCACT GTGTTATTGC TGCAGATATT TTTAACAGCA ACACTTTTTC
18151 AGTGCTTTTT GGAGAAAGAT TTGTTAGTTA AAATGTGGCA TATTGTTGGG
18201 TGGTTTTTAA AGAATTGGAA ATAGCCACAA CATTTGGGTT GTGGCTATCT
18251 CAGTCCTTGA AGACATGAAA TATCAAGTAA AGGTTTGTAG GTGTTTTGGC
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FIGURE 3F

18301 CTGTTCTGTC TTCCACGGTT TTTAAAGAAC AGCAATTAGG TTTGTTGCTG
18351 AAATGCAGTA AATGCTTTAT ACTCCTTTCC CCAGATCTTC CTGTCTATGG
18401 ACATGGCCTG GCCCTTGTTG GCCTTCATGC CCTGTCTTTA CTCTGGAATG
18451 GGCTGGGTGT CAGATTATTT TATTCCACGC ATCCATAGTC CCTCTGCTCC
18501 TGCCTCACAG CATGACACAG TTGTGCTTAG TTAACGCATT TGTGTAATTG
18551 CTGGTTTAAA GCCTGTCTTC CCTCTTGGCC TGGCAGCTCC AGGTGGCAGG
18601 GCCGGCTCCT CTTCTTCACA GCCACATCCA TGGCATGTAC AGCCTCGCCT
18651 GCTCCCGGGT AGCTGCCCAG TGGACATTGT CGAGCCAGTC AGAATGGCCA
18701 CAGGTAGTGG GGACAGATTG GAGCTCCTTT GCCTAAGAAT TTGAGAAGGT
18751 GACTCCCAAG CAACTCTGCA ATATCAGGAA TCTTGATGTT GGTTTGTCTT
18801 GGCTTCAAGT CCCGGTTCTG CCACTTAGTG TGATTTTGGG CAGGTTTCTT
18851 ATGGAGCCTC AGTTTCCTCT CCTGTCAGAT GGGGTTATTT ATATGTAAGT
18901 AGCTACCCTG CAGAGCTGGT GTGAGGGTTC AATACAGTAA TGCACGTGGA
18951 GCCCATGGAA CGATGCCGGC ACACGGACAG CTCAACTAAG TGTTAGTTGT
19001 TAGATTTAGA TTGTTATTAT CAGAATCTGA TGGGGTGCGG TGGCTCACAG
19051 CTGTGGTCCC AGCCTCTCAG GAGGCTGAGA CAGGAGATGG CTCAAGACCA
19101 GGATCTCCAG CCCAGCCTGG GCAACATAGT GAGACCCTGT CTCTTAAAAA
19151 AAAAAAGAAA TAATGAATCT GCTGTTGCTA AATAGGCACT TAGAATGGCA
19201 CAGTCATTTC TCCTCTTGTC TTCAGTGTCC TGTTAATTTC TTTACAAATT
19251 AAAAAAATGT CGATAGCAGT CTTATTCAGA TACAGCTTCC TCCATCCCTC
19301 CTTGTCTTGG CAGGTGCCTT GCTCTGGGGC ACACATCAAA GCTGTTCTCT
19351 CTGCTGGGTG GCCTAGAAGG ATTAGTCTTC CTTTGCTGCT CCTTTCTTCT
19401 AATTCCCTTC CCCGGCTTCC TCCCACCTGG GCTCTGTGTG TGGCCTTCCT
19451 GGAGAAGGGC AGACGCCAAT GACTCCATGT CTAGGCAGAG GCCTGGGTGC
19501 CTGCACTTCT TGCCCTGTTC TTGGCCTTGC TGTGCTGGGC GGGGGCAGGG
19551 TGGTGTGGGG CATGGGGTGG TGTTGGGCAT GGGGTGGGGT TCTGGCTGAG
19601 GCAGGGCTCA GTGCCAGGCC CAGGCAGAGC TGAGTGGCTC CACTTCTCTG
19651 AGATGGTTGT CAGCATCATA CCTGCTGCTG TCCCGTTAAT TCCCCATGCT
19701 GCTGCTGTTA GTCACCTCCC TAATGGAGCT GGTCTGTAGC TTCTGGGACA
19751 GCTGATTTCC AGGGGATTAT TTGTATTACA CACTTTAATG CTTTTTTAATA
19801 GCAAATTTTT AATTAAATGG AAAGTCCTTT TGGAAGCGAG GGAGCAGCAG
19851 CTGCAGCAAG ACTCAGCGTG AGGCACCGAC TTAGACCAGA GGTGCGCAAG
19901 TGAGTGGGGC GGAGGCAATG GCAGGACTTC GAGAGGACTT GATTGAGTGT
19951 ATATGGAGTG TGCCCAGGCT AATTTTTATG GGAGGAAGGC AGGGGCCTGG
20001 CGCTGGCTCC TTCCTCCTGT CCTAAAAGCC CCCTCTGTCA TCTGCAGGCC
20051 TAGGGAAGCA TCTTCTTTGC CCAGGAGAGA ATGTATATTG GATATATACA
20101 TTATATCCAA TAATGGGAGG GATATTGGAA GTATCACCTG CCTTTGATCC
20151 CGTTCCCAGA AATACTGAGA TTGGGATGGG ATTTTTGGGG TTGAGTCACT
20201 AGATTAGATC AAATAGTGTA GGTAATGGGA TGCGGAAACA GTCTTGAGGC
20251 CCTGGCTCCG GCCCTGGCAG GCTTCGGAGT CCTCAGTCAT CAAGGGAGGA
20301 GAACAAGGGG GCTATAGTGG TGGTTCAGTG CCTCGGGACT GTGCCGGCTG
20351 GGTTGTATAC TTTGCTTTCT GAATGATCTT GCTTCGTGGG GAGGGGACAT
20401 AGGGAAGCAC CTCAGCCCTG AGGAAACGTG TGACACTGGA AATGGAAGCA
20451 GCCAGGGCCC ACCCAGGAAG AGACATGGCC ATTTCTTTGT CTCCTAGCAC
20501 TGAACTGGTT AGTTTGGTGT CAGGCCATTC CTGAAGTGCT CCATGAGGTG
20551 CACCTGTAAC TGCCAAGGCT TGGAGCAAAG GTCAAACCGA GGGAGGCCTT
20601 TGGAACAGAA GTTCCCCATC AAGAGAGTTC ACGTGAGGGG AGGGACAGGA
20651 CAGTCAGCCA AAGCGGAGTC GTTTCTGCAT TAGAATGATG CTCAGGGGTT
20701 GGCATTTAAC CCAGAGGTGG CTTTGTGGGC AGAAACTTGA AGAGGAGACC
20751 TCAGAAGACT TCAGGTTGGT TTTTTACCCA AGAGCTTTGG AGGCGGGGAG
20801 CAGGGAGGGA TTCCGCCTGC CAGCTTTTTC TCGCAGCTGG TGCATCGCCC
20851 GAGTCTTCTT CCAGTGGCAC CCTCCCGGAC CTGTCTGCGA TGCTGCTTTA
20901 GGGACATTTG TAAGTGGTCT TTCTTTTGGA TGCCAGGGCT TTGTTGCCTG
20951 AATATGGGGG CTGCCCCACA TTTCTTAAGG GAAGCAGTGG TGTAGACCAC
21001 AGTCTTTGGA GTCAGGTAGC ACTGGATTCA CATCTTGACC CACCACTTAG
21051 AAGCTCTTTG GCCTTTGTTA AGAGACTTTG TGTCCCTGAG CCTCTGGTGC
21101 CCTCATCTGT AGAATGGGAA TAACATTCAT CTCAGGTGGT CGAAAGGAAT
21151 AATAAACTCC TCAAAGGCAG GCACTCTGTC TGTTCCTCCT GAATCCCGCT
21201 GCCTAGCGTG GGGTCCAGCA CATAGTAGGT GCTTGATAAA TGCTTGCAGA
21251 ATCAGTAATG TATGCAAGAG CCTAGCACAA GGCCTGGCAT AGTAAGCACT
21301 TAATAAGCTG TTATTGTTGT CATTGCCTGA ATGTGTGCGT GGCCTTCCAG

FIGURE 3G

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21351 GCTCACCATC CATTATCCTG CACCACGTGC CTTCCTGCTG AGCTCTGCCT
21401 TTCCACCTTC TTCCCCACCC CTTAGTTCTG CTCCCATTTA CTGCTCTGGA
21451 AGAGCTCTCT GGCTTTCCCA TCTGGTCATT GTTGTCCCCT GCCGTCAACA
21501 TTGCTAGGTG CTGCTCACGC TGCATCTCAC CATCGTGCAT CATATCCCAG
21551 GACCACCTTC TCGGAGACCA GCCCTCTGGG AAGGTTCCGG CTTTTCTCCA
21601 TCTTGACTTC TTAGCCATGA AGCTTTTCTC TCTTGCCTGA GTCTGAGGTG
21651 GCAACCAGAG CGCCAGGCTC TGGCTCCCAG GCTGCCATAGC CTTGCACTGG
21701 GGGGCACTGG GCACGTCGCC ACTTCCCCCC ACTGCTCCTT CTGGAGAGCC
21751 CTGTGAGCCC GACAGGATGG GGCAGGGGTG GGGCTGCTGA GGAGAAGCCT
21801 AGGATTCCCA AGTTTTCTCT CTGTTAATCT CTGTCCCCAT CTCCTCTCTT
21851 GCAGTGCGCC TCCATGACAG TATTTCTGAA GAAGGGTTTC ACTACCTCGT
21901 GTTGACCTG TAAGTGCCAC TTTCTGAGGG TGTGGGGGCC TTTCCCTCTA
21951 GCTGACTCAA AATGAAGGCT CAGGAAGGGG CCTAAACAGG CTCTCCAGCC
22001 TCCGCCCAGG GCCCCCTCCT TTGTCCGAGG GAAAGGATTT GACTGGGGCA
22051 GATTGCTGCC CCCACCAAGG GGGTCTCCAT GTTCCCCCAG CGTCCCCCCA
22101 GGGCTCTGAA CCCCAGGACA GCATTCCTCT CGCACTTCTG TTCAGCAGCA
22151 CGCCTTGCAC AGATGCCTTT GTCTTGTTTC TCAGTGTGCT GTCCTTAGTG
22201 AAGAAATAAA AGACAGCTCT TTGCATGACC TTAAAAATCC TGAGAAATCA
22251 GAGGTAGCTT TCATTAGTCG GAAACCAGGC TCCATGGAT TGGGTCTCTC
22301 CTCCACGTTG GTTGTGGTTT AATGTCTTAA AAGTGGCTCT TACCTCCTGG
22351 ACACTCCTCT CCAGGATTCT CAGGGTTGGG TCTCTGTGTC ATTGGTCTCA
22401 TTACTCTTCA ACTTCAGTAG TAGCTCTGTC CTTCCTGGGC AGCGATATTT
22451 TAGTGTTTAT GTTGGTCTCA AAGCTGTGAC TTTTGGGGTA GGTTGACTGT
22501 TTTCTCTTAG ATCCCTGTAT CTTCATCTCT GCCTGACTAT TAGTGAATCT
22551 GTGCATTTTG GAAAAAGAAA TGTCCGGAAG GAAGGGACGG CCCATGATAC
22601 CTCAAGGAGA ATCCGGGTGT CACTGAAGGA TCGAGTGTGT TCTGAGCTCT
22651 CAGATGAAAT GCATGGGGAG TTGGGATTTC TCTGAAAGCC ATTCTACAGG
22701 GTGACCCTGT TTCTTCTTGG ACATTGGGGT TGGACAAAGG ACCCTTTCTG
22751 CCTCTGACCC TCTTCTTCCC GTTGGTTGCA GTGTTACCGG CGGGGAGCTG
22801 TTTGAAGACA TTGTGGCCAG AGAGTACTAC AGTGAAGCAG ATGCCAGGTA
22851 GGATGAGGGC CCGAGAGTTC AAATGTAGCT CTGGAGTTTA GGACTGAAGG
22901 AAGTCTTGGC CACCTTCGGG GTCCAGCATT GTACCTGTTT GAATAGTCTT
22951 TGGGGAAGAT CAGAATAGCT CTTGTCTGGA GAAAGATTCT GTTGAGCTGG
23001 GCTAGGGCTT GCATACTGTG GGTGATATTA GAAGTTAAAA ATTCAGCACT
23051 TCCTAACCAG GCGCAGTGGC TCATGCCTGT AATCCCAGCA CTTTGGGAGG
23101 CTGAGGCAGT TGGATCACCT GAGGTCAGAA GTTGGAGCCC AGCCTGGCCA
23151 ACATAGTGAA ACCCTGTCTC TACTAAAAAT ACAAAAAAT TAGCCGGGTG
23201 TGGTGGTGTG TGCCTGTAAT CCCAGCTACT TAGGCGGCTG AGGCAGGAGA
23251 ATCACTTAAA CCTGTAAGCG AAGGTTGCAG TGAGCCAAGA TCATGCCACT
23301 GCACTCCAGC CTGCGTAACA GAGCGAGACT ATGTCCCCCT CCCCCCCCCC
23351 CACAAAAAAA ATCACTTCCA AATGAATGTT TTACAAAGCT TTTCCAAGTC
23401 TCCTTTACCC TGTGACCCCA GAAATACTTT TTTTTTGCAC TACCATGTAC
23451 TCGCCACCAT GCCCAATGTC CCCCTCTGCC CTTTCTTTC CTTTGACAAA
23501 TTCTGGTGTG CTCAAGCCAC TGTGCTGAGG CTCTGGCATG ATCCAGAGGT
23551 GCAGAAGACA TGGTTTCTGT CCTGAGGGAG TGGAGAGTTC TGGGCTGATA
23601 ATCCAACCAT AGAGCCCCGG GAGCTTTCAG CCTCTGTCAC CTTGTCCCTA
23651 GACCACCATG ACCAGCCTTG CCGTGGGGCT CCTCCAACTT GAGGACCCGTT
23701 CCCCGGCCAC ATGCCTCAGC CTCTGCCCTC CCTGGAATCC CTGGTGCCTC
23751 CCTCACCCAC GCTCTCAGGT GCCTGTTCAG CCTGCCTTTC CCGCCTTGGC
23801 TCTTCCCCCA GCCTTGCTTT TCTCGAGGGT GATGTCCCTA CAACCTGGTT
23851 TTGATCATCC TGCCTGCAGC TTATCTGGCT TATGTGGCAG CTCTGGCTGC
23901 TTCTGGAGAG TGGGGAGTG CAGCTTCCTC ACGAATTCT CAACCTTGAG
23951 AGGCCAATGT TTGCTGATCA ACTTCAGATG CTTCAGCCTC GGGAAGAATT
24001 CTCAAGTGGG GAGATGAATT CCAGTGCCAG CAGGGGAGGA CGAGGCTCTG
24051 GGACGGAGGA GGCAGTGATG GCTCAGGGAG CCTGCGGGGA GGAGGGAGAG
24101 CTATAGGGAG GGGGCCCTGA GGGGGGGTGA CTGTACCAGT GGGCTTGGCC
24151 TGGCTCTGCT GGGACACTTC GCACTTTTGC CATTTTTGGC CAGAAGGCGC
24201 TCCCTGCTAG CCCGGCTCTG TTCTAATTAT ACATCTCTGT GGAGACTCGC
24251 CTCTATAGCT CAGTCTTAAA GTTTCTGTGG CCCACTCTTG GGCTGTGTCC
24301 TATGGGGAGG CCCGAGTTTC AGCCCCCAGG GACCCAGTAC GACCCCTTGG
24351 TTCTTGTGGC ATCCCCAGCA TCAGATTTTA GGAATAGTAA GTCCAGGCCA
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FIGURE 3H

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24401 CCCAGCCCCA TACACTGGGA TGCTCTGCAG ATGTGCTTAA TATACCAGAT
24451 AGTGCCTGAT GACGGGGGTC TATATTCTAG GCCAAGTTCC TCAGCCTTGG
24501 TGCTACTAAC GTTTTAGGCC AGGTACTTCC TTGTTGTGAG GCCTCTCCTG
24551 TGCATTGTGG CAGACATTTA GAAGCATCCT TGGCCTCTGC CCACCAAATG
24601 CTGGGAGCAC CCCTCCTCCA GTTGTGACAA CCAGAAATTT CTCTAGGCAT
24651 TGCCAAATGT CCCCTGCCGT GGGGGGGGGC GGGCGGCAAA TTCATTCCCA
24701 GTTGAAAACC ACTGCTCTAG ACTGCCCCCG CTCCCTGTCA GGAGTTTGAT
24751 GACAGGGATG GCAGGATGGT TTGCTATGTG GACAGTCTGA TTTACGTGTG
24801 TGACTGTGGC TGGGCGCAGT GGCTCACGCC TGTAATCCCA ACACTGAGAG
24851 GCCAAGGTGG GTGGATCACT TGAGCTCAGG AGTTCAAGAC CAGCCTGGGC
24901 AACATGGTGA GACCTTGTCT CCACAAAAAA ATACAAAAAT TAGCTGGGCA
24951 CGGTGGCTCA TGCTTGTGGT CCCAGCTACT GGGGAGGCTG AAGTGGGAGG
25001 ATTGCTTGAG CCCAGGAGGT CAAGGCTGCG GTGAGCTGTG TTCACGACAT
25051 TGCACTCTAA CCCAGGCAAC AGAGTGAGAC CCTGTCTCAA AAATAAAATA
25101 ATAAAATAAC TTTGGGTTTT TTTCTCTACG CAAAATCATC AGAAGTGCTC
25151 CTTAAATGCC CTGTTTGGAA GCTCTTAAGT ACATTGTTTC TTAAAGGTAT
25201 CTTTGTACTT GTTTTAGCTG CCTTACTGGA TGCCAGACCT CAGGGCAGCT
25251 ATTGGGTCTT GTCCATCTTC ATTATCCTAG GCACTCAATA AACATTTAGG
25301 GAAATGAATG AGTGCACCCA CCGCCAAAGT AGCTTAGGTT GTTTAGTTGG
25351 ACTCTCCTTC CTAAGTTGCC AGCACAAGCT TCTTCTCCAA GAACAAAGTT
25401 ACTGTATGGA GAAAGAGAAA GAAGGAAGGG ATTGGATGCT CTCTTCTTCC
25451 TCAGGATTCT GGGCTGTCTC CTGATCTCTT GGAAATGAGT TGGTTGTGTT
25501 AGACCTTTCC AGTCAAAAGG GGGTGAGAGG AACCCGTTCT AGCGGTGATC
25551 CTAGAAAAAC CATTGCATCT GCCTGGGCCT CGGTTCCTC TTTCTTTAAA
25601 TAGGTTGAAC AAGATGATGT GCAGAGTCTA AGGTTCCAGT GGCCGTTAAG
25651 TGATTCTCTG TGAATCCGTG GCCCCTTGTC ACATGCCTTA GTCTGCAGCA
25701 TGTGGTTGTG GATGTGGATG AGGTGGTTTA ACCCTGCGCT AACATTTCTT
25751 TTCCTTCTGC TTTTTTAGCC ACTGTATACA TCAGATTCTG GAGAGTGTTA
25801 ACCACATCCA CCAGCATGAC ATCGTCCACA GGGACCTGAA GGTACTACCC
25851 AGGCTCCCCT CCGTGCCTCT GCTCATGAAG TGTTGGCGCC ACCTGGTGCC
25901 AGATAGTGGT ACTGCGTAGG CCCAAACTAG GCTTCCTCTG GGCTGCAGGG
25951 TGGGTGCTCA CAAGGTTCTC TGTGTTTCTT CTGCAGCCTG AGAACCTGCT
26001 GCTGGCGAGT AAATGCAAGG GTGCCGCCGT CAAGCTGGCT GATTTTGGCC
26051 TAGCCATCGA AGTACAGGGA GAGCAGCAGG CTTGGTTTGG TAAGGGTGAT
26101 CCTGTCTTCC CGGAATGCAG CCCCCGCCCT TCCTCCTCTT CCTGATCTGC
26151 CTTCCTCTAT TAGAACTAGA AGCCAGACCC TTAATGGTCC TGGCCTCCGA
26201 GATCTCTCTT GGCCGGTACGC GACTCAGTAC AGTAAGTCTA GCTGTTGTCA
26251 GCACTGCTTT CTTGCTGCCT GTGGGAAGGA GCTGGAGTTC CTGGTAGGCA
26301 TACGGCTTTG CCGTCTGGTT CAGATTCCAG GCGCTACAAG AAGCCCAGCC
26351 TGTCAGCTCT TGCTGCCCAT GTGCTGAGAG TTTATGTAGC AAAAGCAGCA
26401 GGAATAAGAT GGGACTTGGG GGAAATGGCT GGTGTGGATT TAACGAGAGA
26451 GAAAGTGGGT TCAGTATGCC TCTGCCCTCT CTTTTGCTAC AGGTTTTGCT
26501 GGCACCCCAG GTTACTTGTC CCCTGAGGTC TTGAGGAAAG ATCCCTATGG
26551 AAAACCTGTG GATATCTGGG CCTGCGGTAA GCCCATTCCA CGCTCTCAGC
26601 TTTTCGCTGT TAAGGGCCCT CAACTTCCGA TGATGGCAAG AAAGAGGCAT
26651 CGCTATTCCT TGCAGGTCAC ACACGTGCCT GGTGTATGTG AAATTATGGT
26701 GTTTGCCCCT GGGATGGCTG TTCCCATCAC ACCCTCCTCC CTGCGTACTT
26751 CTGGGATGAC ATTGTATCCT TCTTGGAGAG GGATTTGCCC ACGCCTTAGA
26801 GGATGGGTTG TGCCTAAAGA AATCCCTGGT GTGACTTGGT GACGTGAAGT
26851 GTGAGGCATA GCAGGAGGGG CTGGTAGCAT AGCATTATCG GCTGGCATCC
26901 ACTTCTGACT CTGGTATGGC CCCTGCCTTT CTAGGTGGCT CTGAGCCCTG
26951 CATGGTTTTT CTTGGTTCCT CAGGGAAGTA GGCGACTGAC CCCCATGACC
27001 TGTGTGTTCT GTCTCGTAGG GGTCATCCTG TATATCCTCC TGGTGGGCTA
27051 TCCTCCCTTC TGGGATGAGG ATCAGCACAA GCTGTATCAG CAGATCAAGG
27101 CTGGAGCCTA TGATGTAAGG ACCAGAGAGC CGGGCAGCCA GGCCAGGAAG
27151 GGCAGATGTC CTGCTCCTCG GGCTCTGTCC AAGGGAGCAG GCTTGTTTAG
27201 TGTGTCACGT GATACGGGGG TGTCAGGGGA CTTTGAGGAC CCAGGAATGG
27251 GCATCCAGGG CCCAATTCTT GCCACTCTAT GTCCCAGGGA GCAACTTTCT
27301 TTTGCACAGC CTTCTTCATA ACTAAAATTG AGGAGTCCAC TGAAGTCCTT
27351 TGATCTTTAC TTGCAAAGAA TGGAGCGGCC TCATTGGTGT GCTGTGTAAC
27401 ACAGGGACAA AAGGCCTGGA GACTCCCTCC ACTGCAGTGG CACCTTGGAC
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FIGURE 3I

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27451 ACATTGCTGA GCCTCTGTTC CCTCCTAAGT ATAGAGCTGG GCTTAAACCA
27501 GAGAATGTTG GAGTCCCCTT CCCGCTCTAA TCTGATGTTC TGGCATTCTA
27551 AACATGACTG TTCTGTCTGT CTTTCCAAGT CTTTAAGTTG ACACAGGTTC
27601 TGGAATAGCC GCAGGGCTTC TCCAACTCTG CCAGTCACAG CTTTAGGTAC
27651 CACAGAGTAT CCCAATTACA GGAGTTGAGT TGAAGACAGA ACCAGTGTTG
27701 CAGGGTATGA AGCTCACCAA TACCACATTC TTCTCCCTAT TCCTGCTCCT
27751 TAGTTCCCAT CACCAGAATG GGACACGGTA ACTCCTGAAG CCAAGAACTT
27801 GATCAACCAG ATGCTGACCA TAAACCCAGC AAAGCGCATC ACGGCTGACC
27851 AGGCTCTCAA GCACCCGTGG GTCTGTGTAA GTGTCTTTGC TAGTGGCCAA
27901 GGAGCTCAGG GGTGTCAGCC TTCTGTGTGC CCTCGGCACC ACCCCCTCCT
27951 TCTTACCAGC AGAGATTCAT TCTGGGCCCC AAGCAATAAC TGAGCAGCCG
28001 GGCAGAGGAC TGTTGAGGGC CAGGGTCAAT AAATGTCACC AGGGAGACTC
28051 GGGAGGCTGA TGGGGCTGGT GGGCCACTGC TCCTCTCTCC CCCACTCATG
28101 GCTGTCAGGC TGGGATTGGT TCTGTTCTTG GATGAGGGCT CAGGTTGACC
28151 CTTGTGGACT CCAGGTAGCC GGTGATAGAA AGCAGCTGGC AAAACCCAAA
28201 GTGAATTCCC AAGCTGGGGT TCATACTCAG ATCTCAACTC CACTGGAGTG
28251 GTGACCAAGA TCCAACAAAT CAACAGAAGG GGTTTCTGAG TCATTAAAAG
28301 CATAAAAGCT GAGGCATAAA GCTTCTGCGC TAAAGTCCTA GGAGAGTCCT
28351 CTAGGCTATC AGTGTGGGTT GACGTACTCT GTTTTTATAC ACAATTCTTT
28401 CAAGCTGAAA TATCAACTTT CAGACAAAGA AGAGGATTTG GTAGAGTTAG
28451 GCATCTTGAC AACCACGAGG CATTATTTAT CTGTCCATTC TGTGTTTATT
28501 AAATACCTCT TTGGTGCTGG TTACCGTCTG GGTGCTGGAG ATACAAAGAT
28551 GAATGAGGCA TGGTCCCTGC CCCAAAAGAT CATCTAGGGA GACAGGCACT
28601 CAAACAGGCA GTCATGTTAC AATGTGACAA GTAGGTACAA GAATCTAATG
28651 AGAGTACAGG AGCTCCTACT GTTCCTGGTG GGTGGTGGGG TTACTGAAGG
28701 CTGCACGGAG GAGGTGCACC CCCTGTGCTT GTTCTTGGCA AATAACGAGG
28751 TCCTCAGAAC GTTAACCTGC AGACAGAGTT TAGCACAGTG AGAGGTTATG
28801 GGAAACTATG GTGAGTTGAA GGAATGTTGA GTTGTTTGGT TGTCGATGAG
28851 GCTGCAAATA TCAGAATGCA AGAGAATGGG GCAAAAGATT CCCTGACATA
28901 CAAGTTTCTG CCTCAGGAGT TTGGATTTTA TTCTGAAAAC ATAGGGAATC
28951 ATTTAAGGGT TTTAAAGAAG AATGAAATTT GCATTTAAGA ACACTTTGGA
29001 AGTTGTGAGG AAATGAATTG CCAGGCATGG TGGCATGTGC CTGTAGTCTC
29051 AGCTGCTGGG GATGCTGAGG CAGGAGGATC ATAAGCCCAG GAGTTTGAGG
29101 CTGCAGCGAG CTATGATTGC ACCTGTGAAT AGTCATTGTA CTCCAGCCTG
29151 GGAAAGATGG TCAGACCCCA CCTCTTTAAA AAAAAAAAAA AAAAAAGAAG
29201 GGAATTGAAA ATTTTTAAAA GAAAAGGGCT GGAGACAGAG AGCTCAGGAA
29251 GCTTTTTTAA TAGTTGGAAT AGTCTAAGCA AGACCAGGTG AGGTCTCAGC
29301 AGAGGGTAAG GATGGGGGAA TGTGCAGTGT GTTGAAATTC AAGAGATATT
29351 TGAGAGAACC TAAAGGATTT AATTCTCTCC AGTTGGATTT GGGGGGAGCA
29401 AAGAAGAGAG AGGCCAGGTT TCAAGTTGAG CGGAGAGTTG TACCCTCACT
29451 GACCCAGAAG AAAACCAGAG GAGGAGCTTG TTTGTGAGAC AAGACGATGG
29501 TTTTCTCTTT TTTTTTTTTT TTTTGAGATG GAGTCTCGCT CTGTCGCCCA
29551 GGCTGGAGTG CAGTGGCGCG GTCTCACTGC AAGCTCTGCC TCCCGGGTTC
29601 ATGCCATTCT CCTGCCTCAG CCTCCCGAGT AGCTGGGACT ACAGGTGCCC
29651 GCCACCACGC CCGGCTAATT TTTTGTATTT TTAGTAGAGA TGGGGTTTCA
29701 CCGTGTTAGT CAGGATGGTT TCGATCTCCT GATCTCATGA TCCACCCGCC
29751 TCGGCTTCCC AAAGTGCTGA GATTACAGGC ATGAGCCACT GCGCCCGGCC
29801 AAGATGATGG TTTTCATTTT GTGCCTGCTG AGTCTGGCAA CCTCCAGCCA
29851 GACACATTCA GTGGGTGGTT AGAAATATGG TCCTAGAGAT TAGAAAAGAA
29901 GCTAAAAATT GGAAATCCAC ATTGTAGTCA TTTCTGTGTA GTTGGTAGTG
29951 AGGCTGTAGA AATAGCCTCT TCCTATGCTG TAGATGGGCC TGTTCCTATG
30001 CTGGTTGAGT TCTTACGGTG AGCTTCTATT GGCTGTAGTA GAGAAGAGAC
30051 GGCCACTACA CACCAGCATT TAATGATAGG GAGAGTTAGG GGGCCCAGCA
30101 AAGAGCACTG AGAGTGAGAC CTTCCAGAAG ACCCAGAAGC TAAGAAACAG
30151 GGGGTCTCAG TAAGGGAGCG TCAGGAATCA GATGCAGAAG AGTCCCTGAT
30201 TAAGTTGGGG AAGAATCCCC TGGCTCTGAC CATTAGATGC CATTGTTTCA
30251 TCATTTCACT GAGACAGTGG AGAGAAAGAT GAAACCCTGT TTTCAGTGAG
30301 ACGAAAAGGG AGTGAGGGTG AGGAGGGGCA TGGGGAGCTA GGCATTGAGG
30351 TGGGAAATAA ATGGTGATAC TTAGATTAAG ATGGGCCAGG GGAGCTTTTA
30401 ATGTAAGGCT CACACCTGTA ATCCCAGCAC TTTGGGAGAC CAAGGCAGGC
30451 GATCACTTGA GGCCACGAGT TCAAGACCAG CCTGGCCAAC ATAGTGAAAC
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FIGURE 3J

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30501 TCCATCTCTA CTAAAAATAC AAAAAATTAG CTGGGTATGT TGGTACACAC
30551 CTATAATCCC AGCTACTTGG GAGGCTGAGG CATGAGAATC ACTAGAACCC
30601 AGGAGGTGGA GGTTGCAGTG AGCCAAGATA ATGACACTGC ATTCCAGCCT
30651 GGGTGACAGA GGGAGACTCT GCCTCTAAAG AAGAAAAAAT TTCTTTTTAA
30701 AGATTATATT GGTCAGGAGC GGTGGCTCAC ACCTGTAGTC CCAGCACTTT
30751 GGGAGACCAG GGTAGGTAGA TCACTTGAGC CCGGAAGTTT GAGACCAGCC
30801 TGGGCAACAT GGCAAACCC CATCTCTACA AAAAAAAAAA CTTTAAAAAT
30851 TAGCTGGTTG TGGTAACGTG CCTTAGCTAC TTGGGAGGCT GAGATGAGAG
30901 GATCACCTGA GCCTAGAGAG GTGGAGGTTG CAGTAAGCCA TTATTGTGCT
30951 ACTGCACTCC AGCCTGGGCA ACAGAGTGAG ATGCTGTTTC AAAAAAAAAA
31001 AAAAATTTTT TGTTTAAGG AGAGGCTTAA CTATAATCTA TAGAGAAGAA
31051 TCTAGTCCAG AGGAAAGAGT TGAAGATCCT TGCTAATTGA GGAAGCAAAG
31101 GTTTGGACAG CAGAAAAAGA GAGGGGGCTC CTGAGCCAAG GGCAGGGGGT
31151 CCATCCCGGG GATGACCATG ATCCCCCTGA GACTTCTATT AGTGTGGAGG
31201 CAGGTGAAGA TCGGCTTGTG AGTGGAAGTC TGAGCTGAAA GGGGTTCTTG
31251 CTGATGACCT CTCATTTTGC TTTTGGAGAA ATTTACACCG AGGAGGAGGT
31301 AAAATGAGAG ACTTGGGGAA GGTAGAGAAG GTGGGGAGAG TTGCCTCCGG
31351 ACCTGGAAAG AGTGGGCCAA GGGTGAGGGA AAGGATGCGA GGAGGCCCCG
31401 TAGTGTTGGT GGGCACCTGG CTGCAGGTGC CAGGATTTGT TTTTCTGACA
31451 GGCTGGTGAA GACAGCAACA GCAAGGGGAG AGGGCAAGCA ACCTGAAACA
31501 GGCACCCAAG AATGGGGGAA ATATTCTGTT CTGGGGTCAT TTTTGCAGGC
31551 CCTACCCTCT GCAGTCCCGT GTGTCTCGAG CCCCTGAGGA CATCACTATA
31601 TTCTGAAATT ACATAATGAT GCTGGTATTG ACAGCTGAGT CATTGAGGAA
31651 GTGTAGACTG TGTCCCATGG ACTCTGTTTA AGGAGGCCAG GAAGTTAGCA
31701 GTAAATACAT TGAAGACAAA TTTCCATCCA AAAAAGGCGG GGCACAGTGG
31751 CTCACACCTG TTATCCCAGG ACTCTGGGAG GCCGAAGTGA GCAGATCACT
31801 TGAGGTCAGG AGTTCGAGAC CACCAGCCTG GCCAACATGG CCAACCCTGT
31851 CTCTACTAAA AATACAAAAA TTAGCTGGGT GTGGTGGGAT GTGCCTGTAG
31901 TCCCAGCTAC TCGGGAGGCC AAGACAGGAG AACCTGAGAG GCGGAGGCTA
31951 CGGTGAGCCG AGATTGCACC ACTGCACTCC AGCCTGACTG ACAAAGCGAG
32001 ACTCCATTGC AAAAAAAAAA AAAAATTACA TCCAGAATGA TGAAAGAAT
32051 TGATGCTTCA AGGTGACGAT CCTTAGCTTC TGGGATCATG GCTTCATTCA
32101 GGACCTTGCT GGGGGTGTGT GGAGAGGGGC TCTTGGAAGG AAGGAATGTC
32151 CTCTGTAGAG AGCAGGAACC CTGCCGTTCT CTCGCTGCTG AGCATCTGGA
32201 ACGCAGTAGG TGCTCAGTAA ACAGCTGCCT AAGGAGTGAC TGAATGAGGA
32251 TCACAGCCCC CAGGGTACTC TCCTGTTCGG TAGCCTCTGT TTCCCAAGGA
32301 AGAATAGGAC GGTCTCTCAG CAGCCCGTCT AGCATCCGTT ATGGTGTTCT
32351 CACGTTCATG TTGTCCTTAT GTAACCTTGA GTTTCGGGTA GTGCTTTTAT
32401 TCTAAAAGCG TTTTCACATC TGTGACCTCA TTTCATCTTC AGAGCAACTC
32451 TGGGGTGGCT GAGTGCATGA CCCTGTCCTG GGCATGGTAT CGGTGCCAGG
32501 ACTGTGGGAG GCGCAGAGGA TCTGGGCTGG GGCTCATAGC CTGTCTGTTT
32551 GGTTTCTAGC AACGATCCAC GGTTGGCATCC ATGATGCATC GTCAGGAGAC
32601 TGTGGAGTGT TTGCGCAAGT TCAATGCCCG GAGAAAACTG AAGGTGAGTG
32651 TCGTTTCTAG GCTGCCAGCC TCCTTGACAT CATGCCTTGC ACCAGTGTGG
32701 CTCCTGCCCC ATTTCAGAAG GAAGCTCCCC TCCTGGCTGG AGCTGGGCTC
32751 TGAAGGTTGT ACATGTCACA GGGGAGGGGG CCCAGAGGCC TGATGTCTTC
32801 AGGCTCTAGC CAGGACCTGC CTTTGCCTGA GACCAGCCTG CCCTTTTCTA
32851 GGGTCTCAGT GAATTCACAG GACCTTCCTC TTTCCCCAGG GTGCCATCCT
32901 CACGACCATG CTTGTCTCCA GGAACTTCTC AGGTATGTTT TCCCAGCTGT
32951 GTACTTTGAT TATGCCGAGG TGAGTGGATC AGGAATGGGC TGTTGCCATC
33001 CCGGGCACCG CTGGGTTTCC TCGGCGTCCT GGGCCACACC TTGACCAGGG
33051 CGAGTGAGGA TCCTGTTTTG AGGGGCTGCT GCTGCTGCTG AGTCCTGCTC
33101 CTGAGATTCA GGGGGCTGGA CTCACATTTG TGAATTGTTT CCTAGAACTT
33151 CCCAAGGAGT AGCCTGCCCA ACTTGCTATG TACCTTGTTT CTCTGGATTC
33201 TTATTTAACT CTCTGAAGAC TCTCAGCACT TTACAGATTT TAGCCATTCT
33251 AGGATCTTGG AGGATGTGCT GGGGGAAGAA AAGAGAGATG AGGTACAGTG
33301 AGTCTTCTCA ATTGCCAAAT TGCCACCATT CATTTGCCTG CTGGGACGAT
33351 CTCTTACTTC ATTTTGTCCA AGTGGAGATG ACTAATAGAA ATTATTCCAG
33401 ATGTTTAAAC CTTTTGTTGGC GACTTGTGCT TAAAATAGTC CCTGAGATAC
33451 TAGCTATAAC AGTGAAGAAA TAAAGACCAG CAGGAGAGAG GGAAAGGAAC
33501 TTGCTTAAAT TTGCATAAAG AATTGGGAGA GGTGGGACCA ATAATTTGTA
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FIGURE 3K

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33551 AATCATACTT GACATTTATT TTTAAGATGC AAGACACTCC ACTCCCCTCT
33601 TGCCCCCACC CTCACCCCAA CCCCTATTAT TGTTTGCCTT CAATTGGGAA
33651 GCACAGTGGC TTTTTTGTGA GGAAAAGATT AATGTCGAGA CTGAAGACAG
33701 AGAGGGCTCT GCCCAGCTTG CCATCTCCCC CGGTCCTCCC TCCCTCTAAC
33751 CCCTTGCCTC ACTGTTTTGG TTCAAGACCC CCCCTTCTCC TTCCCATAAT
33801 AAGACTCCCT CCCTTGCCTTC CCCTCTGCAC CACCATGGAA AGGGGGTTGT
33851 GTGGGAGCCT AAGCCACCAC TCAGTGGGAG CCACTTCGTGA ATACCCGTCC
33901 TGCTGGGCTC GCCTGCGCTG GCTCCCAGGTA ACGCCAGGGC CTTGGCTGTG
33951 AGGATGCTGC AGGCAGGGAG CCTAGGGCTT CGTGGTGTAG CCTGAGAGCC
34001 ATGGAGCTCC GGAAGGCCAG GGCTGGATAG TGACCCCGGG GCTGGTGGTG
34051 CCCTGCCCTA GGCCTTCTCC TTTGACCCTG GTTTGGGGCT TGATCTTGTG
34101 TCATGGGTAC CCACGACGGG CATACTGTGG TGTGGCTCCA CCTCTCGCAG
34151 ATGGGAACAG GGAAGCGTGG CTGGCTGCCT CCGGTGGAGT TGCAACTGTA
34201 GTCCCACACT TGCTTCTTGT GCTTTAATGA CGCAGCTTCT ACTTTTTGGG
34251 TCTACGAGCC TTTCCAGAGG ACATTGAAGG GCGTTTCGGT GTTGCCCCTA
34301 GAGCGAAGCT CTGTCCTCTC TCCCCTCTGA GTTGAAGAAA TGTGAAGACA
34351 GTCTGCTGCT TCTCTTTTAG CCCAGCCAGT CAATAGCAAG GGCCCTGTCT
34401 TGCAGCCCCG GGCCTCCACA TCAGCCTCCC CCTCCATTTC AGGAAACTGG
34451 CATCCTGGTT TCAGGAAATC GGGTGTTAGG ACAAAGCATT TTATTCATCC
34501 CTGTAGAGCC TCCTGTTCTT ATTGGCCAGA CCTAGACTGG CCTTTGAGCT
34551 CACTTTGCCT TGGGTCAGAG GAGACAAACA ATGTTGCAAG CATTCCAGGA
34601 TGGCCTCTTC TGCCCTGACT CTGGGACAGG TGAGGACAGA GTCTGTCCGG
34651 AAGCTTCTGC AGAAAGAGGT GTCTATGGAT GCAATCAAGA AGGAAGGGCA
34701 CCTGTGTGTT TCTCTAGGGC TGTTTTTTGA GTTGACCTCC AATAGGAGAT
34751 GTGGCTTATC CTGGACTCTA GCAGTTTGGC TAACAGCGAA TCGGGGCCTC
34801 CAGAGTGTAT TGCTTCAGCA GCCTTTGTTT TCTTTCTCAG GGTTTATTTC
34851 TTGGGCACCT TTCACCTCAG CACACTGTGA CACACAGACT GAGAATGCTG
34901 CCTCTCTCGG CTACCTCCCT TAAGACAGGG ACCTGTGTCT CTGAGCGGTT
34951 GGGGGGCATG GAGCTGGGGC CCACCAGTAA ACTTAGCTGC ACAAGGGCCA
35001 CAGACCCTCC CTGGGACCCC CACGCCAGTC CCTCTAGTGT GTGGGATGTA
35051 GAGAGGGGAG AGGGCTGCTC TGCGCCCCCG GCACTCTCAT CGTGGGCTCA
35101 TTTAGCTTCT AGGGAGGGAA GGACTAGAAG GGAGGGCGTT TCATCACAGC
35151 CTTAAGCTAG GGCCGGGCTA CCTCAGAAGG GGCACCTGCC TCTCACCGGC
35201 TCAGGCATTT CGCTGTGGAC CCTCCTCCGG AGGGGGTCAT GAGACAGGCA
35251 CTGCAGCCCT CTCCATCTGG TGGGGACGCA GTGTTCCCTA TGCCCTGGCC
35301 CAGCCCGGTC TTTCCCAGGCC CCCAGACTGC TGCAGGGCTG GCTGCGCCTA
35351 CCTCCTCAGC CTGCCCCTGG CGCTCCGCTC CCCCAGCTCG GCTGGCTTGG
35401 CCACGCCGCC TGGGCTGCGC CTCGCGCTGG GGCATGCTCG CTGCTGACGG
35451 CCCCGTGGCT TTGCGGGGCT CTGTGCACTG AGAGACTGTA TCCCCTCAGT
35501 TGGCAGGCAG AGCTCCGCCC CCGCCTCGCC TGCCGCGAGC GCCGCCGGCC
35551 TGGCCGGGCA AGGTACGTGG CATGAGTCCT CCCCGACCGC CTGCCTCGGC
35601 CCCCTGCCAC CCCACCAGGA GGGCCAGCAT GCCGGGCCCA CTCACCAGGG
35651 AGGCGAGTCC CATGCTTGCG GGCTGAGATG GGCATGCCAG ACAGACTACC
35701 TAACTTGGCA TCTGCAAGCG CATCGTTGTT ATGGAGCCCC CTAACCAGCC
35751 ATGCATGCTG GGCGCTTGCC AACTTTCAGG GGGCAGTAGC CTGGGGGCAT
35801 GGAGCTGGGC AGCGGGGAGCC TTGCCAAGAG CCCGATGCCC TGGGAGGGCT
35851 GCAGCCAACA GTGGGCCCTC AGAGACAGTG CTGGGCATTG CCCTGAGCTG
35901 CCCGGTGCTA GGACTAGATT TCCGCAGCAC TGTTTAAGAC CCCACAGAGG
35951 AGCCGCGCTC CTCAAAATTG TGAAGTCTGG CGCTTGCTGG CCTCCAGGTC
36001 TGAAAGGCTC CAGAGTGCAG AAGCCTCAGA GCCAGCTGTT TCTGGGTTCA
36051 CATCCTAGCC CTGCCACACC CTGAGCGAGT CACACCAGCT CTCCCAGCCT
36101 TAATTCCTCA CCTCTCCAAT GGGGATGATA AATAACATGG TGGTGCTTAA
36151 GATCACCCTG TCGAAGGCTC TCAGCCCTGC CTGTGCAGTA CAGCGTGTTAC
36201 CTGGGAGCTC GTAAGAAGTC CTAATGCCAG GACCCCACCC CAGACAATAA
36251 AATCAGACCC TTAGGGATAA GATAGGTAGT ACGCTTTTTT TAAGCTCCCA
36301 GGTGATCCTA GTGGGCAACC AGCGTTGAGA GCTGGCTGGT GAATGGAAAG
36351 CACTTAGACA GTAGGCGGTC AGGCACAGGA GTCAGCACAT TTAAAAAACA
36401 ACATTCAAAC CCAGCACGAC AAGATAAGAT CAAAGGTCTT TTTCTGGAGT
36451 CAGAATTCTC GTAATGGAAG GACCCCTGTT CTCACTGGAG AGAGATGGAA
36501 CACAGCTTGG GGAGGAATGG CTACCCAAAG GGCAGGAGGG TGGCAGCAAT
36551 AGTGACAACG ATGGTGGACA CTTACTCAGT ACTTGCTATA TGCCAGGCAC
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FIGURE 3L

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36601 TCTAAGTGCT TTTCATGCAT AATCCCACTG GATTCCCACC ACTGTTTTGT
36651 GATGTCAGCC CTACTTTATC CCATTTTATA GATAAAGAAA TTGAGGCTCA
36701 GAGAGGTTAA GTAACTCACC AAAGGTCACA CAGCTGGCAA GTGGTGGAAC
36751 CAAGATACAG ACCCAGGGCA GGCAGTCCAG GTGTATCAGA CAGTTGGGCT
36801 GATTCCATCT CCCTGTGCCT CCCAGACTCT CCTCCCCACT GTCTGCTACC
36851 TTCCTGTGGC CTTTTGTGGC CAGCTGGTGT CACCAGCCTT CTGGCACAGA
36901 GCTCATCAGC CTGGAGCGTC ACCCTATGCC TGGCTAGAAT CTGTTTGACA
36951 GCTCATTATT CTGCCGAGTC CTTCCTGCTC ACAGGTCCAG AGAGTGGACA
37001 CTGGGGAAAG GGTGGCAGCT AGGACCCAGT GAACCTGGTG AGGACCTGCT
37051 CAGTGAAGGC TTCAACCCCC TGGCAAAACC CTCCTGTAGG TGGTCCTGGT
37101 TTCTGTGTCT GTGTCTGTCT GTCCTCTGGT CTCCTGTGTG AACTGTGACA
37151 CTCTGCTTCT TGAGAACACT CAGGAGATGT CTTGCATCCT TGCAGTTTGG
37201 CCATCCAGAG AACTTCCATG GCACCTAGGG ATGGAGCCCT CACTCTTTCA
37251 CCCTGGCACT CTGCTTCCAG GCCTGGGTGG AAGCTGTCAA AGGCAGAGTC
37301 CCCAGTGCCC CAGGCGGCTC CAGTACTGAG CATGGTTTCT CCTCTAAGTG
37351 TCGTGCATCC ATGCCCTCCT CCACGCAGAG GAGATCCTGA GGTGCCACCC
37401 TGAGGGCTCT GACGCCACTC AAGATCCCCT TCTTGCTGAG AGGCTATAGG
37451 AAGTGCCTCT TTTGGGGGTT TCGGGAGACC CTTGGCCCCC TTGTCAGACA
37501 CAGCACTCTC TTGTGGATCT GGCTGCCGGA CTTCAGGTTG GGGAGAGGGT
37551 ACAATGCAGG AGACTTGATA TTCCTCTTTG TTTTCACAGC TGCCAAAAGC
37601 CTATTGAACA AGAAGTCGGA TGGCGGTGTC AAGGTAAGTG TCTCCAGCCT
37651 CTGAACAGAC TGGCCTCTTT CTCCCCGCAG TCACTATGGG AATTCTTGGC
37701 ACCTGGTTCC CCCTTTCCCA GGGAATCTTC CTATCCTTGC TAGTCTGCTT
37751 TAAACCAGAT GCCTTTGTGC TCAGAACAGA AGGTTCTGCT GGCCTGAGAG
37801 GGAAGTAGGG AGGTATTTTT CCTGGCCCTA GCTGGATGGG AATGACTCAG
37851 GGGAAGTGAT CCAAATCATA GTTTATACCA GAGCTGAATC CGGAACCTGA
37901 CTTCTACACG GATGCTTCAT CTCCAGGGCT TGACTCTGGG TTTTTTAGGT
37951 CATTGGTTA TCTTTCTTTT TTTCCTTTTT AGAGCACAAA TCCTTTTAAT
38001 CAAATGAAAG CCAAATTTGC CTGAGTGATT CAGGCAGGGT ATAGGGCTTG
38051 GAACCTGAAA CCACTCTCCT TTTGGTCTTT TTCCTTCTCT CTACAACACT
38101 TTCAGATCCC ACTGAGTGCA ACAGCCTCGA GCTTTCTTGA CGCATAGGCT
38151 CCTCAGAAAA AGGCAAAGGC CATGGTGGAT CACGGCTTGT TCCCACTGGG
38201 TGAGGGAGCT TTTCCCATGG GACTGGGGCA AGAGGAGGGA CCTGGGACCC
38251 ACCAGGAGCC CTGCTGGGAA TGGCTGCTTG GCCAAGGTAG AGGAGAGGTG
38301 ACTGGGGCTA CCCACAGGGC CCAAGACATT CTGTAGATGC TTTGGGGGCA
38351 GAAAGGATCC TGGGGCTAGG GCATTGGGTA GGAGCTCATG CTATCTTGAA
38401 GCCTCCCAGC TTACACTCTA GACTAGATTT TCACTGGGCC TTTTCCCAAG
38451 ATCTTGTGTC AACAGCTGAG ATACACACAC AAGCCCCGTT CCCTCCCCGT
38501 TCCCTCCCCA CTCCCTCCTC TTTCCCTCAT TCTCTGCATG CCTGCTTCTG
38551 TGTTCTTCCG CCCCTCGCAG GGGAGCCTGG GCTCCGCGCA CACCCTCTGA
38601 CATGGAGCTG GGGGCATCGT GCGGTCCCCA AGCTCTGCCC CTGAGCTACA
38651 TGGATGGAGC CAGGTGAGGA AAAGGGGCAG GTTTAGTTGG AGAGAGTGTT
38701 TAATAAGTAC CTGTCAGTCA GATGTCCACG CAGCATTCTG TTCTGAGGGG
38751 TACACAACAG AGGTGTAAGA GGGGGTGTGG CTTTCAGTCG CCATAGGAAG
38801 GGGGCCGCAC CTGGAGTCAG CTGAGCGCTG CTAGTGGACC CACGCGAGAT
38851 GGTTTAGTCC AGGAAGCTCA TAGGAGAGAG CGTACTGGAG AAAGCTGCAG
38901 GGACATAGGT GAGACTCACT TTGCAGTTTT ACTTTCTGCT ATATGTTTTC
38951 TTTAAATTGA AAATATGGGT CAGGCTTGGT GGCTCACTCC TGTAATCCCA
39001 GCACTTTGGG AGGCTAAGGC GGGTGGATCA CCTGGGGTCA GGAATTCAAG
39051 ACCAGCCTGG CCAACCTGGT GAAACTCCGT CTCTACAAAA ATACAAAAAT
39101 TAGCCAGTCA TAATGACCGG TGCCTGTAAT CCCAGCCACT CGGGAGTCTG
39151 AGGCAGGAGA ATGGCTTGAA CCTGGGAGGC GGAGGTTGCA GTGAGCCAAG
39201 ATTGCGCCAT TGCACTCCAG CCTGGGCGAC AGAGCAAGAC TCCGTCTGAA
39251 AATAAAGAAA AGAGAAAAGA AAACAACATG ACATTTCTAT AACTTAAAAA
39301 CAACAAATTA TATTTGTATG GGTTCTCTTA TACATATTGA TGTTCTCTGC
39351 CCAGTGAGAA CACAGGGTGT GTGGTAGATT GATGTCAAAA ATATGGTTGG
39401 ATCAGTCTTA TCAGGCAGAA TTGGAAGTTT CTGTGTCAGA CCATGGGAAA
39451 TACCATAGGC CATTGAGCAG GGAAGCTATG GTGAGAGTGC TGATAGAAAT
39501 GATTTGGCAA GCCGGGTGCG GTGGCTTCAC TCCTGTAATC CCAGCATTTT
39551 GGGATGCTGA GGCAAGAAGA TTGCTTGAGT CCAGGAGTTT GAGACCAGCC
39601 TGGGCAAAAC CTTGTCTGTG AAAAAAAAAA AAAAAATTA ACTGGGCATA
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FIGURE 3M

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39651 GTGGTGTGCA TCTGTAGTCA CAGCTACTTG GGAGGCTGAG GTAAGAGAAT
39701 TGCCTAAGCC CAGGGAGTTT GAGCCTGAGG TGAGCCAAGA TCAAGCCACT
39751 GCACTCTCCA GCCTGGGTGA CAGTGAAACC CTGCCTCAAA AAAAAAAAAA
39801 AGATACCTGC TGTGCCCCTA GAAGTTGGGA AGGCAAAACT TAATCTACCT
39851 TTTAAGGTGT TTACAGTGGG AGAGACACAA GGCAGCTACT GTTTCTATGG
39901 AGTCTGCTAA GGTCTCAGGG AGGTGTGCAC CTGGCAGGTG CTGGGGGAGC
39951 AGACAGATAA ACATCCAAAC CAGGACAGGA ATCTTCTGGA AGGAGATGGC
40001 CAGGAATTGA GCTTGAGGGA GTAGCTGGAT TTTGCTGGGT TAAGGAGGAG
40051 ACAGGAGGGG AGGGATATTC CAGGCAGAGG GAAGAGCGCA TGTGAAGATA
40101 CACGAGGTTG AAACAGCATG ATGATTCTGG GAACTTCAGT ATCTTCTTTA
40151 TGGCTGAAGG GAAGAGCAAT TGCATAAAAT GAGACCTGAA ATAAAGCAGT
40201 GACTGTTGAG GTGGAGGGGA GAGGATGGAA AAGGCACCAT TACAGAACAG
40251 GTTTCTAGCC AAACTTTCTA GATACTACTG GTGTCAAAGA TGAAGGTCAT
40301 GTGCAGCCAT GTAAGATTAG CCCAAGGAGC CAGCTCAAAC CATGCACATC
40351 CAGGGCCCAG CTTGGAATTC ATGTTCTGGA GGCCTTGGCT GGGAGGCAGA
40401 ATCTGTGAAT TTTAAAAACA CTTTCATGAA TCCAAAGCAC ATGAAGGTTT
40451 AAGAGTCTGG TAAAGGCAAA ATTTTGGGGT TATGTGTTAA GAAAGGGCTG
40501 GAACAAGAGT CGGCAAAGGA AACAGAGGAA GGACAGAGAG GTAGGGGGAA
40551 AAGAGAAATG TGCAGCAGCT GCAGCTCTTC CAGGAACCCT GAGGATGAGG
40601 GCTGGGCAGA CACATCATTA GGTAAAGGCT TTAAATGAGG ACGTGCGTGG
40651 GGAACCTAGC CCTGCAATGT GTTGTGTGTC TGACCCTGAT ATGTGCTCAG
40701 TAAATGAGTT TTATGCCACA TTCTTTTGAG AAAAGAGCTT CAATATCATG
40751 GTGGGAACCA GAGGCCAATG ATCACCCAAA ATTAAAAGGC CAACCGCGTA
40801 TTCGCAGCCG TTGTGATGGG AGGGGTTAAT ATTTTTATTG AAAGAGTTTC
40851 TGTGACAAAT AATCCCTCTT AAAACCCAGT AGAAGCTGGG CGTGGTGGCT
40901 CACGCCTGTA ATCCCAGCAC TTTGGGAGGC CGAGGCGGGT GGATCACGAG
40951 GTCAGGAGAT CGAGACCATC CTGGCTAACA CGGTGAAACC CCATCTCTAC
41001 TGAAAATACA AAAAATTAGC CGGGTGTGGT GGCAGGCGCC TGTAGTCCCA
41051 GCTACTTGGG AGGTTGAGGC AGGAGAATGG CGTGAACCCG GGAGGCGGAG
41101 CTTGCAGTGA GCTGAGATTG TGCCACTGCA CTCCATCCTG GGTGACAGAG
41151 CAAGACTCCG TCTCAAAAAA AAAAAAAAAA AAAAAAAAAA ACCCAGTAGA
41201 TAGGCTAGGT GTGGTGGCTC ACATCTGTAA TCCCAGCACT TTGGGATGCT
41251 GAGGTGGGCT GATCACTTGA GGCCAGGAGT TCGAGACCAG CCTGGCCAAC
41301 ATGGTGAAAC CCCTCTCTA CTAAAAATAC AAAAGTAGC CAGTAGTGGT
41351 GGTGCACGCC TGTAGTCCCA GCTACTCGGG AGGCTGAGAT AGGAGAATCA
41401 CTTGAACCTT GCGGGGGGCA GAGGTTGCCG TGAGCTGGGA TTACACCACT
41451 GCACTCCAGC CTGGGGGACA GAGCAAGACT CTGTCTCAAA AAAAAAAAAA
41501 AGGAAGATAG ATGATCAAAG AAAATAAACT GACAACCTGA AAACAAGGAA
41551 GTAGAACTGG ATAACAAATG TGGAAAAATT TCTAGCCTCA CTAGTATCAG
41601 AGAAATGCAA ATTGAAACAA GGTGCCATTT TTGGACTCTA GTTAGTGATG
41651 GTAGTGAAAA CCAGAATGGT CCTTTCTAAA ACAGCCTGTG TGTCAAAACC
41701 ATAAAAATGC TTCTACCTCT TTTTACCCTG TTAATTCTAC TTCTGAGAGT
41751 TTTTCCTAAA GAAATAATTC AAAATAGGAA AAAGCTAAAA GCAGAAAAAT
41801 GTTGAACATG ACATTATTTA TAGCTGTGGA AAGATTGGAG GCTGGGCACA
41851 GTGGCTTATG CTTGTAATCT CAGCACTTTG TGAGGCCAAG TTGGGAGGAT
41901 TGCTTGAACC CAAGAGCTTG AGACCAGCCT GGGAAACGTA GTGAGACCCC
41951 ATCTCTTAAA AAAAAAAAA AAAATTAGCT GAGTGTGGTG GAACGTGCCT
42001 GTAGTCCCAG CTACTTGGGA GGCTGAGGTG GGAGGATTGC TTGAGCCCAG
42051 GAGGCTGAGG TTACAGCCAG GATCACACCA CTGCGCTCCA GCCTGGGTGA
42101 CAGAGTGAGG CTCTGTTTAA AAAAAAAAA AAAAGAGAGA GAAGAAAAAA
42151 AAGATTGGAG ACAATTTGAA AAGCCAGTAA GGAGCCAGAC ACAGTGGTGC
42201 GTACCTATAG TCCCAGCTAC TCAGGAGGCT GTGGCAGGAC AGAATTGCTT
42251 GAGCCCAGGA ATTCGAGGCC AGCTGGGCAA CATAGTGAGA CCCCCAACTC
42301 TTAAAAATGT TTTTAAATTT AAAAATAAAA AGATTTTTTA AAAGCCAGTA
42351 AATGACTAAA TAATTATGGG AAATCTACTT AATAAACTAT TCAAAGTTA
42401 TTAATTTTCA TGACCGTAGG GATATTTTAA GTGAAAAATA AAGTGCAGAA
42451 ATGTTTTATA TTAAGTGAAG GAAGTGGTAT ATAAAGGAGT ACAGACAAGC
42501 CAGGCACGGT GGCTCACGCC TGTAATCCCA GCACTTTGGG AGCCCGAGGC
42551 AGACAGATCA CGAGGTCAGG AGATCGAGAC CAGCCTGGCC AACATGGTGA
42601 AACCCCGTCT TTACTAAAAA TACAAAAATT AGCTGGGCGT GGTGGTGCGT
42651 GCCTGTAATC CCAGCCACTT GGAAGGCTGA GGCAGGAGAA TCGTTTGAAC
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FIGURE 3N

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42701 TAGGGAGTCG GAGGTTGCGG TGAGCCAAGT GCGCCACTGC ACTCCAGCCT
42751 GGTGACAGAG CAAGATTCTG TCTCAAAAAA TAAAAAAAAA AAGGAGTACA
42801 TACACTATCA TTCTAAATTT GGTTTGAAGA AACGTGTTTG TAGATATTTA
42851 TTCAGTATAT AATATGTGGA TAAAAAAGGG ACTGGAAGAA AGCCCACTAA
42901 GTGTCAACAG TAACTTCACC AGGTGATGGG AATTTGAGAA ACTTTTTTGC
42951 TTACACATTT TTCTGTATTC CTATATTTTT CATCTAGATT GTGCACTACT
43001 GTTATCAGAA TTTTTTTTAA ATACTATTTT TTTTTTAAAG TAAAGCATAA
43051 TACCAGGTGT GGCAACTCAT GCCTGGTAAT CCCAGCTACT GGGAGGCTGA
43101 GGTGGGAGGA TTGCTTGAGC CCAGGAGGTT CAGCCTGGGC AACATAAGCA
43151 AGACTCCATC TCAATTAAAA AAAAAAGAAA AGAGGTAAGA CATGTGCTTG
43201 TATTATTATA TCTTATAATG ATATCTTTTT TTTTGTTTTT TGAGACAGGG
43251 TCTCACTCTG TCCCCCTGGC TGGAGTGTAG TGGTGTGATC TTGGCTCACT
43301 GCAACCTCCG CCTCCCGGGC TCAAGTGATT CTTCCACCTC AGCCTCCTGA
43351 GTAGCTGGGA ATACGGGCAT GTGCCACCAC GCCCGGCTGA TTTTTGTATT
43401 TTTAGTAGAG ACGGGGTTGC CCAGGCTAGT CTTGAACTCC TGAGCTCAGG
43451 TGATCTGCCC GCCTCAACCT CCTGAAGTGC GGGGGTTACA GGCATGAGCC
43501 ACCACGCCTG GCCTATAATG ATATCTTAAA AGATTGCTTT CTTTTTTTTT
43551 TTTTTTTTTT TTTTTAGAC GGAGTCTCAC TCTCACCCAG GCTGGAGTGC
43601 AATGGCATGG TCTTGGCTCA CTGCAACCTC CGCCTCCCGG GTTCAAACAA
43651 TTCTCCAACC TCAGCCTCCC AAGTAGCTGG GACTACAGGC GCGTGCCACC
43701 ACACCCAGCT AATTTTTATA TTTTTAGTAG AGACGGGGTT TTGCTATGTT
43751 GGCCAGGCTG GTCTCGATCT CCTGACCTTG TGATCCACCC GCCTCAGCCT
43801 CCCAAAGTGC TGGGATTACA GGCATGAACC ACCGTGCCCG GCCAATTGCA
43851 TTTTTTAAAA AGACTGGAAG ATTGCTAGGA GTATTAGTGG TTTTCCCATG
43901 CCCCTTCTCT GTTTTCCAAA TTGCTTGTAT TGTGGCTGCA GTCCTTTTAT
43951 AATATGAAAC AGGTAAATAA CAACTTATGT TGTGGCTGCA TCAAAGGGGT
44001 GAGAAACGAA AAGGAGAGGA CAAAGCAAGA TGTGCAGAGT TCGACCTTTC
44051 CAGGCTCTCT CAAAGTCAAG GTTTTGATCA ATGTTATGAG GGAGGCCTGT
44101 GAAGTAGCTC AGATGGTCTT GAGCTTTCAG CATCATGGAT TCTTCTTTTA
44151 GATCCCATCT TCCCTTCCCA ACTCCCCCTT CCTCAATTCC TACTGCTTAA
44201 GTGTCCATAG GGCGATTTCT TTTTCACTGT TCAGAAGCTT TCTGCAAGAT
44251 GTTCAAAATA CTAGCCATTGG TTTGAGCAGC TAGTCTGTCT TGTGTTCTTG
44301 ATTTGGGGGA CTTAGCTTCT ATTTAGATTT CTTTGAAGCT GGATGCCAGT
44351 GACCCAGGGT CTATGGAAGA GTAAGAGCCA CTTGTGAGGA TGACTGAAGA
44401 GGCCACAAAC TCTCAGATCC TGAGAGTGTA GGACAACTTG TGCCTTCTGC
44451 TAGTCCCAGG CCAGAATGGC CATCCTATCT TTAAAAAAGA AAGCAAGCAA
44501 GAAAAACGAA AGGTTATAGT TATTTCCCTA AGTACTATTT GAATTATTTT
44551 GTTAAATTAA GTATGAGAAA GAGGTTTGAA CGCTTTTCCA GCTTAAAATT
44601 TAAAATAAAT ATACAGTTTT TAAGTAAAAG TGAGATATGA TTCTTTAGAA
44651 ATCATCTGGC ATTTAGCCAG GCATGGTGGT GTGCACCTGT AGTCCTAGCT
44701 ACTCAGGTGG CTGAGGCAGG AAGATCCCTT GAGCCCAGGA GGTTGAGGCT
44751 GCAGTGAGCC ATGATCATGC CAGTACTTCA GCCCGGGCAA TAGAGCAAGA
44801 CCTTATCTCT AAAAAAATAA TAAAAAGACC TCACATTTAG ACAATGTCGT
44851 AGTGTGCTGG TTCAGAAGGA GCCCAGCTAT GCATGGCTAA GGGCAAATCC
44901 CTGAATGGAG AAGGAAATTG AAAAATGTTG ACTAACCTGA GAAACAGTCT
44951 TTGGAAAAGG GTGATCTCAG GTTCTCATGC AGGACAATTT AGGAAAAAGA
45001 GAGCAAGCCA GGAGAAGGCT GAGAACTTAT TCCCCATTAG TCAAAAATCT
45051 GCTTTAAGTC AAGATCCTGC AATGGCCTTT CACAACAAGC CCCTGAAAAT
45101 CAGCAGAACA AAGACTGGGC CTGGTGAGTG AGTGCCTACG CAGAGTTCTT
45151 GCTGCCGTGA TTCAGTGCAA GTTAGAAACC TGTGCTCTTC TTTAGCCTGG
45201 GGAAAAACCA AAGTCAGCAA ACCCAGCTCA ACTCAGCAAA CTTTCGTCGC
45251 CTGTATGCTA ACTATAAGGC ATGTTGCTAG GTACTGTGGA AATTGTAAAG
45301 ACACATAAGA TAGGAACCTT CCTGAAAGCA GTAACACTTT AGTTGGGTAA
45351 AGGGATAAGG AGATATACAC ACACACACAC ACACACACAC ACACACACAC
45401 CCCACTACTT ATATATATGA ATATAAGGGA ACTCCTTCTT TTTGAGGGAT
45451 GATTTTCGAA GTAAAATATC ATATTTGAGC ATATTTAAAA GGCCACTGTA
45501 AGGCTGTGTG CGGTGGCTCA CGCTTGTAAT CCCAGCACTT TGGGAGGCCG
45551 AGGTAGGTGG ATCACCTGAG GTCAGGAATT CGAGACCAGC CTGGCCAACA
45601 TGGCGAAACC AGTCTCTCTA CTAAAAATAC AAAAAAAAAT CAGTGGGGCG
45651 TGGTGGCGGG CGCCTGTAAT CCCAGCCACT CAGGAGGCTA AGGCAGGAGA
45701 ATTGCTTGAA CCAGGGAGGC GGAGGTTGCA GTGAGCCGAG ATGGTGCCAC
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FIGURE 3O

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45751 TGCACTCCAG CCTGGGCAAC AGAGTGAGAC TCCCTAAAAA TAAATAAAATA
45801 AATAAATAAA TAAATAAATA AATAAATAAA TAAAAGGCCA ATGTAAAAGA
45851 GGCCTAACTA TATTTAGGTT TTTCTTTTCC TTTAAATCTA ATTCTAAATT
45901 ATGGACCATT GTCAATATTT GTAGCCTCTT TCGTTGATTA TAATAATAAT
45951 CCCTGAAAAT GCCTTCTAAA GAATGCTGGC CGCTTGAGGG CAGGAGCAGT
46001 TTATCAGCTG TGTTTACCTG AAACAGCCCT CAGTGTTTGC TGGGCATTGT
46051 TAAATGAATG TGCAAAAGTT GAACGACAGA CGGACATATT ACAGGGGGAC
46101 CTTACCCCCA GTGAGCTAAT GATGACATTG ATAATTACCC TTCATTTTTT
46151 AGACACAGTC TTCTGGGATA TATTTTCAGT GTTCCACGTG GTCTTCATCT
46201 TGATGCGTCT GTTTCACATG TGAACGTAAA GTTCGTGAGC ATCTAGTTGA
46251 GGCTGAGGAA TCACTGCTTT CAACATTCCC TGTGGCTTAC ATCCCTGCAT
46301 TTTTATGATC ACTGTAGTTT TAATCACTGG CACTCCTGTG TTTCTATTTT
46351 CCACGAATTG CAAAATGCAA TAAAAAATTC AAATATTGTA AACAAGCATG
46401 GCTATACTGA CAAAGGAAGG CCAACATTTA ACTGCTAGGT GATTTTCAAA
46451 AGCTCAGCAT CTTTATGTAA AAAGCATAGT AGGGATGCAG CGAAGTCAGA
46501 AGTCAAATTT TATTAGAGCT GAGGAGAGCC TGTAGTAGCT TTTGCTTTTT
46551 CCCTGGTGGC TGCTCACTTG AATTTCAGAC AGTTCTAGTA ATGAGAGAAA
46601 ATAAATAACA TTACAGGGTG AGCTAACCCT ATGAACCCAG ACCTGTAAAT
46651 TTGTAGCAAA ATGATACTTA ACCTCACAGA CTTGTGTCTT AATCTCCTTA
46701 AGAGGCTTTT TTTGAGCAAG GCTGAGACAT CTCAGAAGAT ACTAAATCTG
46751 TGTCTATGAA CCTGACCACA AAAGAGTTCT TCCCTCCCAG GGTCTGGAGG
46801 GTGTGAGTGC CTGTCGGTCC GTGTGCTGTT TAACCCTCTG GTGCTGGACT
46851 CCGGGTCTCC CTCCGCTCTT TTCTCCCTGA TGCAGAGCCC ACACTGGTGC
46901 GCTAACCTGC AGCGTCTCTG TGCTTCTCTT CTTACCTCCT CTTTCCCCTT
46951 CTCTTTCCCT CTTGCTGTGG TGTGTCCAGA AAAGGAAGTC GAGTTCCAGC
47001 GTGCACCTAA TGGTGAGCCT TGCCTGCCCA CCCATCGCCC ACTCCATGCT
47051 GCCTGTGCCC GCCTGCCAGC CACGCAAACC TGTTCTGCCA CGTGCGTGTG
47101 CCTCACTCAT CCTCACTGCA TGTCTGTGCT GTGTGGGCAG GTGTGGCCTG
47151 TCCTGCCAGG CGGGGGCCAT TGCCCAAGGT CACCCAGTAG CCTAAAAAGT
47201 GGACATTGGA AGGGGTGGTA CGGCACCCCC TGCTGTGGAG CTTGGACAGA
47251 CCCCAGCGAC CCAGGGTAGG ATGTGAAGCT GGTAGGGACT TGGGGCAAGC
47301 AAGGGAGAGA CCCTCACTCT CTTGTCACCC AGAAGGAGAG GCCCTGCTTC
47351 CCAGGCATGA GGAGCTGCTT CCTACAGACT GGCAGCTGGA GGGCAACTGT
47401 GTGGTGGGCA GAGGAGCTGG TTGCAGGCTC CCACTTGTGA GTCTCGCTCT
47451 CCTGGCTCTG CCCCCGTGCA AATCCCATTC TCTCTAGCTG TGCCCAGTGG
47501 TTTATTCTGC CCACCCAGCC CTCGGGGGAC AGCTAACTCA TCTTTCTCAC
47551 GGGACACTGG GCACCAAGGG CAACACAGCA GCCTGAGTCA TTATGAAACC
47601 ATCCATTAAA ACCAGAGGTG GGGCCGGGC GCGATGGCTC ACGCCTGTAA
47651 TCCTAGCACT TTGGGAGGCC GAGGCGGGTG GATCACAAGG TCAGGAGATC
47701 AAGACCATAA CACGGTGAAA CCCTGTCTCT ACTAAAAATG CAAAAAATTA
47751 GCCAGGTGTG GTGGTGGGCG CCTGTAGTCC CAGCTACTCA GGAGGCTGAG
47801 GCAGGAGAAT GGCGTGAACC CAGGAGGCGG AGCTTGCAGT GAGCCGAGAT
47851 CGCGCCACTG CGCTCCAGCC TGGGCGACAG AGCTAGACTC CGTCTCAAAA
47901 AATAAATAAA CCAGAGGTGG GGCCACTTGG GTGACATCCC AGCCCTCTGC
47951 AGGTTTGTG GGCACCCTGG AGTCCTTGCC CCCTGTGAGG GTCTTGGCCT
48001 CAGCTGGGAT TTACAGGTAG GGCAGCCCTC TCTAACCAAC CCCGAACAGG
48051 TCAGCATCAT TCACTGAGCT AGGTGGGCTT TGCTTCTTGG TGGGAATGAG
48101 AGACAGCAGA GCTCCCGTGA GTTTAGACCC ACCGTCTCAC TACTCCTGGG
48151 CCCCCTCTTC TCTAGCCTGT CGCAGTCTGT GGAGTCTTGT TCAGTGGAGT
48201 CACTTGGTGC CTGGCTTGAG GTTCCATGCC TAGCCCTGGG TTTGGGGATG
48251 TCTGAGCCAT TGACAGCAAG CTGGCGGTGG ACGGCTTCAG GTCTGGTCCA
48301 AGAGGCCTCC AGGCAAGAAG TAGGACAGTC AGGATGCTTT CTGTGTATGT
48351 CCTAGGAGAG AAGACACACA TTCTAGCTGT CGATGTATCA TCTGTGCCCT
48401 GTGCAGGGAT GGTAGCCACA CATTTGTCTC ACTGCCTATT GAAGAACTTG
48451 CAGGCATCAG GCTGCTCCTC AGTGGCCCCC AACCCCACTG GAACTCAGTG
48501 AGATGGAGTA CGCTGGTTAG GGAACTATCA GAGGCAAAGA ACATCACATG
48551 GATATGGCTC CCTGCCCTGG AGATCAGCCT TCTTCCTTTC TTCCATCTTC
48601 CCCTTGCCCC TCCCTTGCTG TGCCCCTCCG TGTAATGTTT TTGTTTGTTC
48651 GTTTGCTTTT GGTTTTTTGA GATGGAGTCT TGCTCTGTTG CCCAGGCTGG
48701 AGTGCAGTGG TGCAATCTTG GCTCACTGCA ATCTCTGCCT CCCAGGTTCA
48751 AGCAATTCTC TTGTCTCAGC CTCCCGAGTA GCTGGGATTA CAGGCATGTG
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FIGURE 3P

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48801 CCACCATGCC CGGCTAATTT TTGTATTTTT AGTAGAGACG GGGTTTCACC
48851 ATGTTGGCCA GGCTGGTCTT GAACTCCTGA CCTCAGGTGA TCCACCCGCC
48901 TTGGCCTCCC AAAGTGCTGA GATTACAGGT GTGAGCCACC GTGCCCACCC
48951 ACCCACCATG TAGTTTTGAA AGGCAAGGAG ATATCCCTGG TGGTCATGGT
49001 GCTGTTGGGA ATGTTGGCCT GTGTGTGTGCC TACTCTGTCC TGGGCGGCTGG
49051 ATTCTGGGAC TACAGCTACA GCCCCGCTGG GTTTCACCTG CCCCTCCCCG
49101 GAACACTGCC CTTCTAGCTG ATCAGGCCTA AGATTTGTCA GACAAAAAGG
49151 TGAACAGCAC AGTCCTGACT CTGCTCCCTG AGGTCAGTGA ATGCATTTTG
49201 TGTCTGAAAG GGACTTCCAC CCCCATCCTC TGGACACCAT CTCTTAGGCC
49251 AGGCATACTT TTCTTTTCTC CTTCCTCTT GTTTCAGGCT TCGAGCTGGT
49301 GTTGTAAGAA GGAAATACAG GTGCTGGGTT GAAAGTGCAG CAGGAGACTG
49351 CCCACAGATA GGGGACCAGA GTTTCTGAAT TTTGTTCTGC TTTCTTATAA
49401 ACTACCCCCC TTTTTCCTGT ACAGTGGGAA GAAGATCTTG AACTTCTTTG
49451 GGTCAGGTGT GGATTTTGCA ATGACCTGGC ACCTGGCATA AGCAGAGATT
49501 TCTGGAGGGA TGCTTTAAAA CAAGGCTTTG GGCTGGTCCC ACCTTGAGGG
49551 TGCCCCCAGA GCTAGGTCTC TGGGCCCAC AAATACTTCC TCTGATCATC
49601 TCTCTAGCCA TCGCTCCCAT CTACACAGCG TTATGGAGGC CACCTCAGGC
49651 CTACCTCCTC CAGGCCAGAC CAGGGGGCAA GGGAGGTCTG GGAGTTGAAC
49701 CTGAGTGGCC TTGGGGACTC TGGAGGAACT AAACCATCTG TTTTCTTGTC
49751 TCAGCCACAG AGCAACAACA AAAACAGTCT CGTAAGCCCA GCCCAAGAGC
49801 CCGCGCCCTT GCAGACGGCC ATGGTACCTC CTGACTACAG CTTCTCCGCC
49851 TCTGACCCTG GCTGCCTCCT GCCCCTTCCC TCTTCCTCCT CTTGTGCCCC
49901 CTCCCTGGCC TCCTGGCCTG TTCCTTTCTT GGTCCCCATA GAACTGACTG
49951 CTTTGTGTGC CGCCCTGTAT GCCCCTTCCC CTTCATTGTC CCGCCTGGCC
50001 GCGCTCCATC CCGCATGGCA GAAGTGCTGC TCCTGCTCCT GCTCCTTTCG
50051 CTGGTGGGGG GAAGAGTGAT CAGGGCTCTC AGCTGAACCT CCCAGGCCCA
50101 GCCCAGGACC CCTAGTGGGT CTGCGTGTGG GGCTGGGAAG GTGAGTTGCT
50151 TAGGAAAGGA GAGGGTAGGA GCTTTCTTGG GACCTGAACA TCAGTTCTTG
50201 GAGGCCCCCT TGTAAAACCT GCCTCAGCCT CTCCTTTGCA AAGCCAGAAA
50251 CAGGAAAGAG GGCTGGGGTC CCCACCTCTG GATGGTGCTG AGGTCTCCAG
50301 GCTCCTGGAG TGCCTCATGC TGGCTAAGTT CTCTCTGGGC TCCTCCAGGG
50351 GTTCTGTGTG CTCTTGGAGG TCCCTCTGCT AGTGGTGGCT AACTAGAGAG
50401 TCAGCAGGGG GGTGACTGGG AAAGAGGGAG AGGTGATGTT GCCTGCTACT
50451 CCCCTCCTTG CGGACCCTCA TACCACGTGA CGTGGCGGCG TGGGCCAGG
50501 AACTAGGGAA GGCAGAAGGC GGGCGCAGTG GGCAGCTCTC TGGGCTCAGC
50551 TTGCTGAGGG GGCCTCCTGT CCTGGCTCTT TCTGGGAGAC CTCATTCTTC
50601 TGCCCATGTT CCTGCCTCAC ACATTCCCCG TGATGAACGC TGTGGGCGGG
50651 GCCCGGCCTG TGCCCTCAGT CCCACAGCTC CTCTAGTGTA CCTGCCCCGT
50701 GGGAACCCCA TGTGGAAAGA GCCCTCAGAA CTGACAGGAA TCAGGGACAG
50751 AGGCCCTTGC TGTCAGCCTC CTGGGCACCT GCACCTGCCA GGCCTCTCTT
50801 TCTTACCAGC CCAGTGCTGC TGCCAAAATC CAGGGCTATC CCAGCTGCCC
50851 GGGACCCCAG TTGAGCCGGG ATATTTTGTC TTCTGGAGAT GGCTGGTGGG
50901 CAGGCCTCAG TGGTCATCAT AGGGTCTGCG GGGGTCCTGG GGTGCAGGTG
50951 GGGCTCCTCA GGGAAGAGCC ATAGTCTGTC CCCAAGTCGG AAGGGTAATC
51001 TTCATCTTCT CTCACAGGAG CCACAAACCA CTGTGGTACA CAACGCTACA
51051 GATGGGATCA AGGTGAGTGG CTCCTGAGCC TGCCTCCTGC TTTCCAGGTC
51101 AGCAGGAGAC AGGTGGGCTG GGTCCCAGGG GTCTACAGGC TGCACCCTGA
51151 GGCCAAGGTG TTTGCAGAGG CTCAGCTGAA GGTAGCCGT GCCCACAGTT
51201 GCTCCATGCT GAGGAAGGGC ATTATACCTT ACAGAGCTCA GGCTTTGCAG
51251 TCAGACAGAC CTGGTCTGAA TCCTGGCCCT GCACCTTAGT ATCCTTTATC
51301 TGCAAATTGG GGATGATAAT AATAGAATCT TCCTCCATAT GTCGGAAGTT
51351 TAAATGAGAG TAAACGTTCA CTGAAAAAAT AGGCAAGAGT ATCTCCAGAC
51401 CCTGGAGCGT TCTCCATGCC CTGACCCCTT TGTGCCCTTG ATGTTTTCAC
51451 CAGCATTCCT GAACATCTGT TAAGCCCAGA TACCATCCAT GGCTCTGGCT
51501 TACAGAGGTG ACAAGACAAA TTATCTGTTC AAACGGTGGG TGGGATGGGA
51551 GGCAGATAAA AAACCAATAA GCAAACAGAT AAGATAAGCT GGGCACCGTG
51601 GCTCACACCT GTAATCCTCA CACTTTGGGA GGCCAAGGTG CGGCAGATCGC
51651 CTGAGCTCAG GAGTTAGAGA CCACCTTGGG CAACATGGTG AAACCCCTGTC
51701 TCTACTAAAA TACAAAAAAG TAGGCAGGTG TGGTGGCGCG TGCCTGTAGT
51751 CCCAGCTACT TGGGAGGCTG AGGCACGATA ATTGCTTGAG CCTGGGAGGT
51801 GGAGGTTGCA GTGAGCTGAG ATCACGCCAC TGCACTCCAG CTTGGGCTAC
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FIGURE 3Q

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51851 GCAGTGAGAC TTAATCTCTC AAAAAAAATA AATAAGATAA AATCTAATGT
51901 CAATAGGTAA TCTGAAGAAA ATGGCAGAAA GTAGAGAGAG GGCCAGGTGC
51951 GGTGGCTCAT GCCTGTAATC CTAGCACTTT GGGAGGCCAA GGCGGGCGGA
52001 TCACTTGAGG TCAGGAGTTC AAAACCAGCC TGGCCAACAT GGCAAAACCC
52051 CATCTCTACT AAAGATACAG AAATTACCTG GGGATGGTGG CACATGCCTG
52101 TAATCCCAGC TACCTGGGAG GCTGAGGCAG GAGAATCGCT TGAACCTGGG
52151 AGGCGGAGGT TGCAGTGAGC TGAAATCGTG CCACTGCACT TCAGCCTGGG
52201 CGACAGAGCA AGACTCCATC TAAAAAATGA AAAACAGAAA AACCTCACCA
52251 AACTAGACAG AGAGAACAGG GCCTTGAATT AAGTAGTCAG GAGAGGGCTT
52301 CTTTCAGGAG GTGATATCTG AGCTAGAAAC TGAATGGTGG GTGGGAAGGA
52351 GGCAGCCAGG CCAGCTCTGA GGCTGAGTGC CCTAAGCAGA AGGAACTGAA
52401 GCTCAGATGT GGCCTTTGTA ATCAAGCAGA GGGAAGAGCA AAGTGAGACG
52451 GGGAGAACCA TAGGAGAGTG ATGAGGTTGG AGAAGCAGCA GGGCCTGCTA
52501 CAGAGGCCCT TGTAGGAGTT TGCATTTTCT TCCAGCAGCA AGGAGAAGCT
52551 ATTGGGAGTT CTTAGCAGGA GTAACAGAAT CTAGTTGACA CTTTAAAACA
52601 CCACTCTGGC CTCATGATCA AGAACTCTAG GGAGGCCCGG GCGTGGTGGC
52651 TCACGCCCGT AATCCCTGCA CTTTGGAAGG CCGAGGCGAG TGGATCAGCA
52701 AAGGTCAGGA GCTCGAGACC AGCCTGGCCA ACATGATGAA ACCCCATCTC
52751 TAATAAAAAT ACAAAAATTA GCCAGGCATG GTGGCAGGCA CCTGTAATCC
52801 CAGCTACTCA GGAGGCTGAG ACAGGAGAAT CACTTGAACC CGGGAGGCAG
52851 AGGTTGCAGT GAGCCGAGAT CATGCCATTG CACTCCAGCC TGTGCAACAA
52901 GAGCAAAACT CTGTTTCAAA AAAGAAAAAC TCTAGGGAGG AGGTAAGTGT
52951 GGAAGTTAGG GAGACCATGA AGCTGTTATC ATGGTTCAGG TGTGAGATGC
53001 TGGTGGCCTG GAGTCAGGTT GTAGCTGTGC ATTGGAAGTG AAGAGGTAAG
53051 ACATGGGGTT TACTTTGGAG GCAGAACCAG AAGATTTTAT TTTAGATTGG
53101 GCGATCTGAA TATAAGGGAA AAAGAGAAAG AGAAGGATTG AGGATGACTC
53151 CAGGTTTTAG CCTGAGTAAC TGGGTAGATG GTGGCATTTA CCAACTGGGA
53201 GAAGACTAGG GAGGGGATTT GGGAAGAGTC AGACAGCCAG GGTGGAAGCA
53251 GAACCTTCCA CAATTCCTCC TTGCACCTCT TGTAGGAGCA GAAACTCTGC
53301 TTTTGTTCTG CTTTGCTCCT CTGGCTTCCA AGGGATGGAG CATATAGAAA
53351 CATGTTCTTT TTGGCCTACA GGGCTCCACA GAGAGCTGCA ACACCACCAC
53401 AGAAGATGAG GACCTCAAAG GTAGGTGCTG GCCCTTGGAG GGGGAAGGAC
53451 TCCAGCAGTG ACCCAGGTAC CTGGGCTCCA ATGGGGCACC TGCCTTTTCT
53501 GTCCCCAGAA CTGGGAATGC TGGCTCCTAT GCCCCTAGGA GAGGGCTTGG
53551 TATAAAAGCT ACTTTCCACG AGCCAAGATA TGAGGCCCCT GTCTGGTGTT
53601 GCTGAGTTGG GCAAGAGGCT TCTCTTCTTT GACCCCAAGT CTAAAATAGC
53651 TAAGCTAGAG ATTCTCCAGG GGCCAGGGCT CAGAGAACTG TTCCTGTTGC
53701 TGATAATGAT GTGCCATCCA AGAACAGGGG TACCCCAAGT CCCTGCCGAA
53751 GTAGCCTGTA AGTGCTATGA GTCATAAATA GAGTGACCAA TCACTCCTGG
53801 TTTTCCTCGG ACACAGAACT TTTGGTTTTA AGACTGTGAT GGGCCAGGAG
53851 TGCTGGCTCA CACCTGTAAT ACCCAGAACT TTGGGAGGGC CAGGGCAGAA
53901 GGATTGCTTG AGACCAGGAG TTTGAGACAA GCTTGGGCAA CATAGCAAGA
53951 CCTTGTCTCT ATTAAAAAAA AAAAATTAGG AACAAATAAA TAGGCCAGGT
54001 GCGGTGACTC ACACCTGTAA TCCCCACACT TTGGGAGGCC GAGGCAAGTG
54051 GATCACTTGA GGTCAGGAGT TCAAAACCAG CCTGGCCAAC ATGATGAAAC
54101 CCCGTCTCTA CTAAAAATAC AAAAAAAGGC CGGGCGTAGT GGCTCACGCC
54151 TGTAATCCCA ACACTTTGGG AGGCCAAGGT GGGTGGATCA CCTGAAGGTC
54201 AGAAGTTCAA GACCAGCCTG GCCAACATGG TGAAACTCCA TCTCTACTAA
54251 AAATATAAAA AATTAGCCAG GTGTGTGGGCA GGTGCCTGTA ATCGTAGCTA
54301 CTCGGGAGGC GGAGGTGGGA GAATCGCTTG AACCTGGGAG GTGGAGGTTG
54351 CAGTGAGCCG AGATCACCCC ATTGCACTCC AGCCTGGGCA ACAAGAGCGA
54401 AACTTCTTCT CAAAAAAAAA AAAAAAAAA AAAAAATTAG CCGGGTGTGG
54451 TGGCGGGGTC CTGTAATCCC AGCTACTCGG GAGACTGAGG CATGAAAATG
54501 GCTTGAACCC GGGAGGTGGA GGTTGCAGTG AGCTGAGATT GCACCACTGC
54551 ACTCCAGCCT GGGTGACAGA GCGAGACTCT GTCTCAAGAA AAAAAAAAA
54601 AAAAATATAT ATATATATAT ATATATATAT ATATATATAA ATATAAAACC
54651 CAGATAGTCC TGGGAACACT GGGATGAGTT GGTCACTCTA GTCTTAAGAT
54701 TTTGGCCTGA ATGATGGAGT TGGAACTAAT CTGACAACCG TGAGGCCACA
54751 TTTGGTCATG TCCTGGTGGG CCCGTAAGGA CCACTAGCCT AAGCTTGGGC
54801 CTGGCTAGAG TGCCAGGGCG GTGGGAGGGC ATGGCAGGCT GGACCCCCGG
54851 GAATCTCTGT CCTGCTCTTT GATTGGGCCT CCTGGAATTG CTCCCTTTGC
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FIGURE 3R

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54901  CTGAATTCAG  TAAGTGACCT  TGGGCCAGGA  CATCAGAAAA  GACAGAGGAA
54951  CACTCTAGGA  CAGAGCTGGG  AGAGCATGCC  CTGGGTGGCA  AGGGGGCACC
55001  AAACCTTTTG  GAACCAAAAA  AAATAGCAGA  AAGCTGCGAG  GAAGTGAATC
55051  ATAGTAGCTC  CAGGCCCCTG  TGAGTGAGGT  CAGATCAGTT  TTGATTCCGG
55101  CACTGCTGGC  AACATAGGAG  GCGCTGTCAC  TGCTGGGCTC  TGGACCCTGT
55151  GGCCTGGCCC  CCTGGAACAT  CTTCCCCGGG  ATCAGGGGTC  CTTGGACAGG
55201  CTGTTGTAAG  GCTCGTCTGG  AAGCCACAGC  CCAGGTCTGG  GCACCTGCCT
55251  GGTGCCCTCA  GCTGGGAGGC  CTCTCTGGCA  GAGGCGGCGG  CGTGGGATGT
55301  CGTCCAGTGT  CCACAGCAGC  CTGAGGCGAG  GCGTCCCCTT  GCCCCGGCTC
55351  TACAGCGCCA  TGGGCTCGGG  GCCTGTCTGG  CTTGCTCGCT  CACCTGCCTT
55401  GTTCTGTTTG  TTTTGGCTGC  TCTGCCTTGC  CCTGCCCTGC  CCTGCCCTGG
55451  CTGGCTAGCT  GCCCCGCTCC  GCACTGGGAA  TGGCAGCTCG  GTGCCTGAAG
55501  GACGGAGCTC  CCGGGACAGA  ACAGCCCCCT  CTGCAGGCAT  GCAGCCCCAG
55551  CCTTCTCTCT  GCTCCTCAGC  CAGTAAGTGT  GAGGGAGGCA  CATTCTGGCT
55601  TCCGTCTCCC  TGGCTCGTCC  TGAAGCCCCT  CAGGGACCCC  CACCACAGCT
55651  GTCAGTCCCA  CCCACCTGCC  CGTGGTAGTA  AGCTCTGGGA  GCATGGCCTC
55701  TGCTGGGGGT  GGGGGGTAGA  CTGGAGGTGC  TGTTGAGACC  AGGCAGGGGC
55751  CCCTGAGTCT  GGGGCCCAAA  GAAATATGAG  AAGTGTGGGT  GGAAAAACAT
55801  GGCCTGGGAT  GAGGGGAGTA  GAAAGCCCCC  AGGATGTGCA  GTGGGCCTTG
55851  CCTCAGCGCT  GAGCCAGGAA  GAAGGGCAGA  GTCGGAAGTC  AGGTCTGTGG
55901  GGGTGGGAGT  GGGATGATGG  GGAAATCGTG  ACAGCGAGGA  ACTGTGTTGG
55951  GGATGTAGTG  CTTCCTGAGT  CTCAGCATAA  CAGTATTAAG  AGCATGGGGT
56001  CAGAGGCAAG  ATAGATCTGA  GTTTAAATCC  CAGCTACACT  GCCTTCAAGA
56051  GTGTGAAGTT  TAACCTCCCA  GAGCTGCAGG  TTCCTTATCT  GTAATGTGGA
56101  AATAAAATGG  CACGCACCTC  AGAGCCTTGT  TAGATAAAAG  ACAAGGCAGT
56151  AGGAAGTCTT  GATACGGTGC  CTCGATGGGT  TATCAGTAGC  TCATCCTCAT
56201  ATTTCTAGTT  ACGTCTGTGC  TGGAGGATGC  CTTTGTCTGC  TGCTTTTCCT
56251  CCCACCATCT  ATCCTTGCAG  AGTTTCTAAG  CACAACCCTC  TTCGCCCGTG
56301  GGGCCCCAGT  CAGGTCATCC  AGATGGGTCT  GGTGGGGTTG  GAGAGGGTGT
56351  GTGTGTGTGTG  GGTGCACACC  TGCCTGCTGC  TTTTGGAAGC  CGATCGAACT
56401  CCTTGCTTCC  CTTAACCTGC  TGCTTGCTCA  CCTGGAGCTG  TGGCCTAGCG
56451  GGGCTGACGG  CTGTGGGGCC  CCCTCCTGGA  TGTGCCTTTG  GCTGCGCTGC
56501  CCTGTCCCAA  CTGTGCTGCT  TGGCTGTGCT  GGCCCGGCTG  GGCCGTGGTG
56551  GTGCTGTTCT  AACGCTTGCA  GTTGTCTTGC  AGCCTTTTGC  TCCTGTGAGG
56601  AAAGGGTTGT  GGCCTGGCCC  CGCCCAGGCC  TCGGGTTAGG  ATGAGCCCAA
56651  GCTCAACCCA  AGCTCTCCCT  TACCCTGGTG  GCAGCCCCTG  CTGGTAGTGG
56701  CATTCCCTAT  AAGAGAAGCC  CATGCCGGCA  GGACATCACC  AGCTGTCCCT
56751  TGGCTTTGGA  TGGGTTGGGG  AGGAGGCCTC  TGGAGGGCAC  CACCTCTGCC
56801  TGCCTGTCAG  TCTGAGCCCT  GTCTGGTTTT  CCTGAGGAAC  ACGTCCTGGC
56851  AATGAGAGCT  GGTGTGAAAT  GTGCAGCTTT  CCCAAGCCTC  GAGAGGTAAA
56901  TGGAGCAGCC  TCTCTGGTAC  AGGCTGTCCC  AAGTTTTTAC  AGTTCTGGGA
56951  TCATTTCTCC  CAGAAAAGCC  CTGTGGAGTT  GAGCAGTGGG  AAGCATCCAT
57001  CCTAGGGTTC  TGATGGTCTT  TTGGCACCCC  AGCCCTAGCT  GGATTCTGCT
57051  GTCAGGCTAC  CTGTCACCCA  GGGCTGGGTC  CTGGCCACTG  AATGAGGGCT
57101  ACGAGTGGGG  GTGGTGATTG  AGACCTGACT  GAGCCCCTTC  AGGTGAGAGA
57151  AGTAAATTGG  GGGTGGAAGC  GGCCTTATTG  GGAGATGCTT  GTGAGAGAGG
57201  CTGCTCATAC  AGGGGAGGGG  CTCACAGCAT  TCACGATGTA  CCAGGCTCCT
57251  CACCTGTTAA  AGGCAAGCGT  GTTTTCTGCA  ACCTGGTTGT  TGATGGAAAG
57301  GGAGGCAAAG  GCCAAAGAAC  CATAACTAAT  GGCTGGGCTT  CAGGAGAAAG
57351  TGGTCATTGT  CTCTGCAGAC  TGCAGAGAGG  GAGACGGGAG  GGAAGGTGTG
57401  TTCGCTCTTC  CTGCCAAGGG  CCCTAGAGAC  AGAGAAGAGG  GATGTCTTTG
57451  TCATAAGCGA  TCACAGGGGA  CTCCTGAGGA  CTGGGGAGGG  CTCTCTGTAA
57501  CTTGGGAGGT  TCCCCAGTAG  GTAAATTGAT  GGATTTTTCT  CCCCCACAGT
57551  GCGAAAACAG  GAGATCATTA  AGATTACAGA  ACAGCTGATT  GAAGCCATCA
57601  ACAATGGGGA  CTTTGAGGCC  TACACGTAAG  TAGAGACCCA  TTTTTTTTTG
57651  TGACCTAAGT  CATCTCCCAA  GGCCTTCCCT  GCTTCCAGAC  AACAATTAGG
57701  ACCCTGGGGA  AAGGGAGGTT  GGACCTGGGG  CAAAGTATCT  GAGTTAAGCC
57751  CTCTCCTAAA  CTGGGAGCCC  TTCCAGGTAG  ATTCCCTGAG  CTCACCCATG
57801  GTATCCTGGC  AGTGGGCCGA  AAGCACAGGG  CTGAGTGGCT  CAGCAGGCAG
57851  GCCTGGAAGA  TCTTTGCTGT  CTTGTCTGGC  ATGGCCACAG  GTAGCCTGCT
57901  GCTACTGGAT  AGACACCGCT  GATAAGGAAG  GAAGACAAGT  CACTCCATAG
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FIGURE 3S

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57951 AAGCCTGATA GGCTGCTTTT TTTTTTCTCC CTGTAGGAAG ATTTGTGATC
58001 CAGGCCTCAC TTCCTTGAG CCTGAGGCCC TTGGTAACCT CGTGGAGGGG
58051 ATGGATTTCC ATAAGTTTTA CTTTGAGAAT CGTGAGTGGG TTCGTGCTGC
58101 TGATATACTC CTGCCTGCCC CTTTACCCCT TTGTCTCTGT CTCCTGCTCA
58151 CCTTCTCATC CCAGTTGCCC ACTTTTCCCT TATTTGACCT TCGTGCTGCA
58201 CTCCTACTCT GTATGCTTGT CCCCTTGTGC CCCGATGGTT GTAGACAGGC
58251 ACCTTTGAAG GCCCTGCTCC TGAGCTCCAA GTGCCATTCA TTCTGCAGCT
58301 GCTTTGTGGC AGTGCCAGTC ACCACAATCA AGCTCACTTA TTTCTTGCCG
58351 GGGCGGGTGG CTTACGCCTG TAATCCCAAC ACTTTGGGAG GCTGAGGCTG
58401 GCGGATCACG AGGTCAGGAG ATCGAGGCCA TCCTGGCTAA CACGGTGAAA
58451 CCCCATCTCT ACTAAAAATA CAAAAAATTA GCCGGGCTTG GTGGCAGTGC
58501 CTGTAGTCCC AGCTACTCGG GTGGCTGAGG CAGGAGAATG ATGTGAACCT
58551 GGGAGGCAGA GCTTGCAGTG AGCCAAGATC AGGCCACTGC ACTCCAGCCT
58601 GGGCAACAGA GCAAGACTCC ATCTCAAAAA AAAAGAAAAA ATTATTTAAG
58651 CCTCACCTCT TTCCAAGACG GATTGGAAGG AAACCCTTTG AGATTAGGTT
58701 GAGATGATCT CAGCACATAA GAACTAAGCT CTGTGTCTGC AGGTTTCACA
58751 ATAGAGGAAA TTAAAACCAG GATAAGAATG TGCAAACCAG GGCACTGTTG
58801 GTGATTTGCG AGATCGGAAG TTGTGGCTAG AATCTTCCTG ACTATGGAGG
58851 AAGGCAGACG TCTTGTATAG GGGGTGGGGT GTACATTCTG GACAGTTCGT
58901 GGAAAATAAG GGGATAAGAA GCTGAATCAT CACCCCCTCC CATCTTTCTC
58951 TCTGCTCTAT GAGACCCTCC CCTTCCTTAT TTTTATCTCT TCCCACTTTA
59001 TGCTGGGCCT TCCCTATCCT GCCCTGAGTT ATAGTTAGTC ACTAACTTCT
59051 CCGCTGGCTC CCACCCTTAT CACATCTCAG CTACATATAT AAACTCTCTG
59101 TTATCTAAGT AATTCTATTA GCCAGAAGCA ATTCCAGAGT TTATATTAGT
59151 ACTAGGAAGG TGTCATGTAG CCCCTGTCTA ACATTTGAAT TGAACTAAAA
59201 TGTGAATCTC AATAAAAGCA ACACAGTTTT CACAGCATAT GCTGATAATG
59251 GCAATCCAAC TTCTTTTGCC TTTTCCCCAG AGAATCCTGG GAATATCCTG
59301 AGCTTGGTGC TTTGATGATT CTATTTCAGC TTTGGTGCCT TAAAAAAAAT
59351 TACAAATCAA TTTTGAATGG TTTAAGTTCA TGATTTTGTT CTGCAGCCCT
59401 AGCTAGGGGT GAGCCAAGCC TTATGAAATC TAAACTCAGC CTAACAGAAT
59451 AGAAAATCTA TAGGCTTTAG TTAAGAGTCA CATGGTCCTG AGTTCAGGTG
59501 TGTGATTTGA GCAAATTATT CCTTGAGCCT ATTTCCTCAT CTTATAATGA
59551 AGAAAATATT ATCCACCAAG AAATACAGCT CGGGCATGTA AAACCCCAGC
59601 ACAATGCCTG ATTAAAAGCG CAGCAGGTAC TGTCACTGTT ACCCATCTTT
59651 CTGTTCCTTT TGGATAAAGG AGACTAATGT AATGTGGCAT CCTGGCCTCT
59701 GGAGGGCGTT CAGGGGTTCG GGGGTGGGGG GGGGCGGTAC TTGGAGATTC
59751 TGGGAGTGGT TGCTTGGGAG ATGGTAAGAC TTGGAAGTGC AGGCTGGGAG
59801 GAAAATGCAG GTGCCCAGGC CTGATGTCCT CTTACCTACC CCACCCTGCC
59851 CTGCAGTCCT GTCCAAGAAC AGCAAGCCTA TCCATACCAC CATCCTAAAC
59901 CCACACGTCC ACGTGATTGG GGAGGACGCA GCGTGCATCG CCTACATCCG
59951 CCTCACCCAG TACATCGACG GGCAGGGTCG GCCTCGCACC AGCCAGTCAG
60001 AAGAGACCCG GGTCTGGCAC CGTCGGGATG GCAAGTGGCT CAATGTCCAC
60051 TATCACTGCT CAGGGGCCCC TGCCGCACCG CTGCAGTGAG CTCAGCCACA
60101 GGTGCACCTG GTTGACGGGG GAGAGGGGCT GGAAGGGCCT GGGATAGGTG
60151 GGGTCAGAGG AAGAAGAGAA GGCTGGGAGG TGGTCCTGGG AGAGGAGGTG
60201 TGGGCCGTCC CAGAGGACTG GCAAAGCCTG GCAGAATGGT TGCAATAAGT
60251 TATGCTTGGA AATCAGACAG ACTAGGGTCT GGCTCCGTGA CTCCAAATTG
60301 GATGACCTCA GACAGGTTAC TTCCCCTCCC TAAACTGTTT CCTTAGCTGT
60351 CAAAGAAAGG CAGAGAGTGG TGCCTACCTC ATTTAATCAT TGTGAGGATT
60401 AAGTAAGATA CTATAAGTAA AGCACTTAGT TAGTGCTTAG CAAATGGGAG
60451 GCAGTTTTGT ATTTAAGCAT TAGCTTCACC CACTTTCCCC ACCTTCTCAG
60501 GCCGACTTGG CCATGTGTTT AGCGTGCTAA AGTCGCTGGA ACTCATCTGT
60551 GTGCTCATTG TCCTCTGTTC TGTTACCACA TTCTGTCCTG TTTGACAGGG
60601 GCTTTAGGAG ATTCCAGCCG GAGGTCCAAC CTTCGCAGCC AGTGGCTCTG
60651 GAGGGCCTGA GTGACAGCCG CAGTCCTGTT TGTTTGAGGT TTAAAACAAT
60701 TCAATTACAA AAGCGGCAGC AGCCAATGCA CGCCCCTGCA TGCAGCCCTC
60751 CCGCCCGCCC TTCGTGTCTG TCTCTGCTGT ACCGAGGTGT TTTTTACATT
60801 TAAGAAAAAA AAAAAGAAA AAAGATTGT TTAAAAAAAA AAGGAATCCA
60851 TACCATGATG CGTTTTAAAA CCACCGACAG CCCTTGGGTT GGCAAGAAGG
60901 CAGGAGTATG TATGAGGTCC ATCCTGGCAT GAGCAGTGGC TCACCCACCG
60951 GCCTTGAAGA GGTGAGCTTG GCCTCTCTGG TCCCCATGGA CTTAGGGGGA
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FIGURE 3T

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61001 CCAGGCAAGA ACTCTGACAG AGCTTTGGGG GCCGTGATGT GATTGCAGCT
61051 CCTGAGGTGG CCTGCTTACC CCAGGTCTAG GAATGAACTT CTTTGGAACT
61101 TGCATAGGCG CCTAGAATGG GGCTGATGAG AACATCGTGA CCATCAGACC
61151 TACTTGGGAG AGAACGCAGA GCTCCCAGCC TGCTGTGGAG GCAGCTGAGA
61201 AGTGGTGGCC TCAGGACTGA GAGCCCGGAC GTTGCCGTAC TGTCTTGTTT
61251 AGTGTAGAAG GGAAGAGAAT TGGTGCTGCA GAAGTGTACC CGCCATGAAG
61301 CCGATGAGAA ACCTCGTGTT AGTCTGACAT GCACTCACTC ATCCATTTCT
61351 ATAGGATGCA CAATGCATGT GGGCCCTAAT ATTGAGGCCT TATCCCTGCA
61401 GCTAGGAGGG GGAGGGGTTG TTGCTGCTTT GCTTCGTGTT TTCTTCTAAC
61451 CTGGCAAGGA GAGAGCCAGG CCCTGGTCAG GGCTCCCGTG CCGCCTTTGG
61501 CGGTTCTGTT TCTGTGCTGA TCTGGACCAT CTTTGTCTTG CCTTTTCACG
61551 GTAGTGGTCC CCATGCTGAC CCTCATCTGG GCCTGGGCCC TCTGCCAAGT
61601 GCCCCTGTGG GATGGGAGGA GTGAGGCAGT GGGAGAAGAG GTGGTGGTCG
61651 TTTCTATGCA TTCAGGCTGC CTTTGGGGCT GCCTCCCTTC TTATTCTCC
61701 TTGCTGCACG TCCATCTCTT TTCCTGTCTT TGAGATTGAC CTGACTGCTC
61751 TGGCAAGAAG AAGAGGTGTC CTTACAGAGG CCTCTTTACT GACCAACTGA
61801 AGTATAGACT TACTGCTGGA CAATCTGCAT GGGCATCACC CCTCCCCGCA
61851 TGTAACCCAA AAGAGGTGTC CAGAGCCAAG GCTTCTACCT TCATTGTCCC
61901 TCTCTGTGCT CAAGGAGTTC CATTCCAGGA GGAAGAGATC TATACCCTAA
61951 GCAGATAGCA AAGAAGATAA TGGAGGAGCA ATTGGTCATG GCCTTGGTTT
62001 CCCTCAAAAC AACGCTGCAG ATTTATCTGC ACAAACATCT CCACTTTTGG
62051 GGGAAAGGTG GGTAGATTCC AGTTCCCTGG ACTACCTTCA GGAGGCACGA
62101 GAGCTGGGAG AAGAGGCAAA GCTACAGGTT TACTTGGGAG CCAGCTGAGA
62151 AGAGAGCAGA CTCACAGGTG CTGGTGCTTG GATTTAGCCA GGCTCCTCCG
62201 AGCACCTCAT GCATGTCCCA GCCCCTGGGC CCTAGCCCTT TCCTGCCCTG
62251 CAGTCTGCAG TGCCAGCACG CAAATCCCTT CACCACAGGG TTTCGTTTTG
62301 CTGGCTTGAA GACAAATGGT CTTAGAATTC ATTGAGACCC ATAGCTTCAT
62351 ATGGCTGCTC CAGCCCCACT TCTTAGCATT CTTACTCCTC TTCTGGGGCT
62401 AATGTCAGCA TCTATAGACA ATAGACTATT AAAAAATCAC CTTTTAAACA
62451 AGAAACGGAA GGCATTTGAT GCAGAATTTT TGCATGACAA CATAGAAATA
62501 ATTTAAAAAT AGTGTTTGTT CTGAATGTTG GTAGACCCTT CATAGCTTTG
62551 TTACAATGAA ACCTTGAACT GAAAATATTT AATAAAATAA CCTTTAAACA
62601 GTCCATTGTG TTACTGCTGT TGGAGGTTTA CGGCCAGAGG CGTAGATTTT
62651 AGCAGCCTGG GTTACCAGGT TGGAGAGAGT ACCTCCTCCT ACTCCCTTTG
62701 GGTACTTTTG AGAATAAAAC TTCCTCATGC CTGTAATCCC AGTACTTTGG
62751 GAGGCCGAGG CGGGCGAATC ACGAGGTCAG GAGTTCGAGA CCAGCCTGGC
62801 TAAT   (SEQ ID NO:3)
```

FEATURES:

Exon:	1690-1694
Intron:	1695-2000
Exon:	2001-2095
Intron:	2096-14208
Exon:	14209-14268
Intron:	14269-21854
Exon:	21855-21909
Intron:	21910-22781
Exon:	22782-22847
Intron:	22848-25768
Exon:	25769-25841
Intron:	25842-25986
Exon:	25987-26089
Intron:	26090-26492
Exon:	26493-26576
Intron:	26577-27019
Exon:	27020-27114
Intron:	27115-27753
Exon:	27754-27876
Intron:	27877-32559

FIGURE 3U

Exon: 32560-32643
Intron: 32644-32889
Exon: 32890-32932
Intron: 32933-35499
Exon: 35500-35562
Intron: 35563-37589
Exon: 37590-37633
Intron: 37634-46979
Exon: 46980-47012
Intron: 47013-51017
Exon: 51018-51062
Intron: 51063-53371
Exon: 53372-53420
Intron: 53421-55458
Exon: 55459-55572
Intron: 55573-57549
Exon: 57550-57625
Intron: 57626-57986
Exon: 57987-58081
Intron: 58082-59856
Exon: 59857-60086

CHROMOSOME MAP POSITION:
Chromosome 10

ALLELIC VARIANTS (SNPs):
DNA

Position	Major	Minor	Domain
1603	G	A	Beyond ORF(5')
8632	T	-	Intron
19366	G	A	Intron
23770	T	C	Intron
31013	A	T G	Intron
33206	T	A	Intron
33263	G	A	Intron
33859	C	A	Intron
37254	T	C	Intron
40809	C	A	Intron
41025	T	C	Intron
42232	T	C	Intron
50477	G	A	Intron
55352	A	G	Intron
55914	A	G	Intron
56633	G	A	Intron

Context:

DNA
Position

1603   ACCCCCACCCGCGGCGCCGAGCCCGGCCACTGCAGCCCCCGCCCCGCCCGCCCGCCCCCCAGA
        CGTTTCCAGAGCTCAGAGTGCGAGCTCCCGTTTGACGGGGACGTCAAGGAAAATAGCATG
        GGAAGGGGAGTTCTTGATGTCTGACTGTGTGTCCTCTCTTCCCTTGCTGTGTCAGTTGAGCCGG
        GATGCAGTGAGATGAAACCGGCTGTGGGGGGGGTTTGAGCCTCACTTTGCCCCATGGTTGA
        GGGAGATTTCTCTTTCAGGGGATGATACCCTCTTTTTAATCTTTCCTTCCCCGACCTTCA
        [G,A]
        CTGTTCCTGCTGAGAGAAGGGCAGGGTCTCTCTGCTCCCTTCTGCCCTGGTTCTCTTGGC
        CGGGACCGCAGGGCTGTCTGAGATGCAGCAGGTGTGTGTTTTCAGCATCGCCCACCCGCT
        CCTGATGTGCAGCCTGAGGTGGAGGCTGTTGCCTTGCCCAGGGACTGGATGAGGGGGTGG
        GAGCGCGGCACGCCACCCACATCTGTTCAGTGTCCTGCGGTGGCCCGCGTCCTTTTGCCTC

FIGURE 3V

ATGTTGGATGGTGGTGGTCACAGCGCCGGTGTGTGTGCATGTACGTGAGTGTGACTAGAG

8632
GACGGCGGCCTCTGCTGCTTGGGAAGAAGATGAAAGGCACTCAGGAGGGCAGCAAGTGAG
GCCGCCTCCCATGGAGCCCTGAAATCAGTGGGGTTGCAGGAAGTTTCTCACATCCATGTT
TAGGGTCATAGGCACAGACCTGCAAAATACCCTTTGCAAAGTTAAGAATGTCTTTGAGAT
TGGAACTTGGGAGAGTCCTCAGTCAGAGTAGGAATGTGCATCCTTTCCCACGTACAGAGG
ATTGTATGTTTACGTGGCAGCAGGATCTTATTTGAAGCTAGTGCTGGCATTTGTGTTTTT
[T,-]
TTTTAGGAAAATGTCACTAAGTCAAGCAGGCCCATCCCTGAGAGGGCCATGGAGAATCTG
TGGCCAGCCCTCCCTGGCCCCCTGACCTGGCAGAGGAAGGAAAGGGCATTGGAGTAGGCT
TCTGTCTTCAGGCCAGAGGGGGAGGTGGTTCAGGGGCAGGCTTGGTGCACCCCTTGGCTG
CAAGCTATCACCTCCCTATCTGCTTCCTCTTTTCTGCCTCCCTGGTGCATCTGGTCACT
TCTTGCTGCCCTTCCTGTGAAATCGTGGCACCTTGGACCAAGTCCTGAAGCACTTGGGCA

19366
CTCAGGAGGCTGAGACAGGAGATGGCTCAAGACCAGGATCTCCAGCCCAGCCTGGGCAAC
ATAGTGAGACCCTGTCTCTTAAAAAAAAAAAGAAATAATGAATCTGCTGTTGCTAAATAG
GCACTTAGAATGGCACAGTCATTTCTCCTCTTGTCTTCAGTGTCCTGTTAATTTCTTTAC
AAATTAAAAAAATGTCGATAGCAGTCTTATTCAGATACAGCTTCCTCCATCCCTCCTTGT
CTTGGCAGGTGCCTTGCTCTCGGGGCACACATCAAAGCTGTTCTCTCTGCTGGGTGGCCTA
[G,A]
AAGGATTAGTCTTCCTTTGCTGCTCCTTTCTTCTAATTCCCTTCCCCGGCTTCCTCCCAC
CTGGGCTCTGTGTGTGTGGCCTTCCTGGAGAAGGGCAGACGCCAATGACTCCATGTCTAGGC
AGAGGCCTGGGTGCCTGCACTTCTTGCCCTGTTCTTGGCCTTGCTGTGCTGGGCGGGGGC
AGGGTGGTGTGGGGCATGGGTGGTGTTGGGCATGGGTGGGGTTCTGGCTGAGGCAGGG
CTCAGTGCCAGGCCCAGGCAGAGCTGAGTGGCTCCACTTCTCTGAGATGGTTGTCAGCAT

23770
CCCCCTCTGCCCTTTTCTTTCCTTTGACAAATTCTGGTGTGCTCAAGCCACTGTGCTGAG
GCTCTCGGCATGATCCAGAGGTGCAGAAGACATGGTTTCTGTCCTGAGGGAGTGGAGAGTT
CTGGGCTGATAATCCAACCATAGAGCCCCGGGAGCTTTCAGCCTCTGTCACCTTGTCCCT
AGACCACCATGACCAGCCTTGCCGTGGGGCTCCTCCAACTTGAGGACCGTTCCCCGGCCA
CATGCCTCAGCCTCTGCCCTCCCTGGAATCCCTGGTGCCTCCCTCACCCAGGCTCTCAGG
[T,C]
GCCTGTTCAGCCTGCCTTTCCCGCCTTGGCTCTTCCCCCCAGCCTTGCTTTTCTCGAGGGT
GATGTCCCTACAACCTGGTTTTGATCATCCTGCCTGCCAGCTTATCTGGCTTATGTGGCAG
CTCTGGCTGCTTCTCGGAGAGTGGGGGAGTGCAGCTTCCTCACGAATTCTCTCAACCTTGAG
AGGCCAATGTTTGCTGATCAACTTCAGATGCTTCAGCCTCGGGAAGAATTCTCAAGTGGG
GAGATGAATTCCAGTGCCAGCAGGGGAGGACGAGGCTCTGGGACGGAGGAGGCAGTGATG

31013
TCAGGAGCGGTGGCTCACACCTGTAGTCCCAGCACTTTGGGAGACCAGGGTAGGTAGATC
ACTTGAGCCCGGAAGTTTGAGACCAGCCTGGGCAACATGGCAAAACCCCATCTCTACAAA
AAAAAAAACTTTAAAAATTAGCTGGTTGTGGTAACGTGCCTTAGCTACTTGGGAGGCTGA
GATGAGAGGATCACCTGAGCCTAGAGAGGTGGAGGTTGCAGTAAGCCATTATTGTGCTAC
TGCACTCCAGCCTGGGCAACAGAGTGAGATGCTGTTTCAAAAAAAAAAAAAAAATTTTTTT
[A,T,G]
TTTAAGGAGAGGCTTAACTATAATCTATAGAGAAGAATCTAGTCCAGAGGAAAGAGTTGA
AGATCCTTGCTAATTGAGGAAGCAAAGGTTTGGACAGCAGAAAAAGAGAGGGGGCTCCTG
AGCCAAGGGCAGGGGGTCCATCCCGGGGATGACCATGATCCCCCTGAGACTTCTATTAGT
GTGGAGGCAGGTGAAGATCGGCTTGTGAGTGGAAGTCTGAGCTGAAAGGGGTTCTTGCTG
ATGACCTCTCATTTTGCTTTTGGAGAAATTTACACCGAGGAGGAGGTAAAATGAGAGACT

33206
CCATGCTTGTCTCCAGGAACTTCTCAGGTATGTTTTCCCAGCTGTGTGTACTTTGATTATGC
CGAGGTGAGTGGATCAGGAATGGGCTGTTGCCATCCCGGGCACCGCTGGGTTTCCTCGGC
GTCCTGGGCCACACCTTGACCAGGGCGAGTGAGGATCCTGTTTTGAGGGGCTGCTGCTGC
TGCTGAGTCCTGCTCCTGAGATTCAGGGGGCTGGACTCACATTTGTGAATTGTTTCCTAG
AACTTCCCAAGGAGTAGCCTGCCCAACTTGCTATGTACCTTGTTTCTCTGGATTCTTATT
[T,A]
AACTCTCTGAAGACTCTCAGCACTTTACAGATTTTAGCCATTCTAGGATCTTGGAGGATG
TGCTGGGGGAAGAAAAGAGAGATGAGGTACAGTGAGTCTTCTCAATTGCCAAATTGCCAC
CATTCATTTGCCTGCTGGGACGATCTCTTACTTCATTTTGTCCAAGTGGAGATGACTAAT
AGAAATTATTCCAGATGTTTAAACCTTTTGTGGCGACTTGTGCTTAAAAATAGTCCCTGAG
ATACTAGCTATAACAGTGAAGAAATAAAGACCAGCAGGAGAGAGGGAAAGGAACTTGCTT

FIGURE 3W

33263   TGCCGAGGTGAGTGGATCAGGAATGGGCTGTTGCCATCCCGGGCACCGCTGGGTTTCCTC
GGCGTCCTGGGCCACACCTTGACCAGGCGAGTGAGGATCCTGTTTTGAGGGGCTGCTGC
TGCTGCTGAGTCCTGCTCCTGAGATTCAGGGGGCTGGACTCACATTTGTGAATTGTTTCC
TAGAACTTCCCAAGGAGTAGCCTGCCCAACTTGCTATGTACCTTGTTTCTCTGGATTCTT
ATTTAACTCTCTGAAGACTCTCAGCACTTTACAGATTTTAGCCATTCTAGGATCTTGGAG
[G,A]
ATGTGCTGGGGGAAGAAAAGAGAGATGAGGTACAGTGAGTCTTCTCAATTGCCAAATTGC
CACCATTCATTTGCCTGCTGGGACGATCTCTTACTTCATTTTGTCCAAGTGGAGATGACT
AATAGAAATTATTCCAGATGTTTAAACCTTTTGTGGCGACTTGTGCTTAAAATAGTCCCT
GAGATACTAGCTATAACAGTGAAGAAATAAAGACCAGCAGGAGAGAGGGAAAGGAACTTG
CTTAAATTTGCATAAAGAATTGGGAGAGGTGGGACCAATAATTTGTAAATCATACTTGAC

33859   TTGACATTTATTTTTAAGATGCAAGACACTCCACTCCCCTCTTGCCCCCACCCTCACCCC
AACCCCTATTATTGTTGCCTTCAATTGGGAAGCACAGTGGCTTTTTTGTGAGGAAAAGA
TTAATGTCGAGACTGAAGACAGAGAGGGCTCTGCCCAGCTTGCCATCTCCCCCGGTCCTC
CCTCCCTCTAACCCCTTGCCTCACTGTTTGGTTCAAGACCCCCCCTTCTCCTTCCCATA
ATAAGACTCCCTCCCTTGCTTCCCCTCTGCACCACCATGGAAAGGGGGTTGTGTGGGAGC
[C,A]
TAAGCCACCACTCAGTGGGAGCCACTTCTGAATACCCGTCCTGCTGGGCTCGCCTGCGCT
GGCTCCAGGTAACGCCAGGGCCTTGGCTGTGAGGATGCTGCAGGCAGGGAGCCTAGGGCT
TCGTGGTGTAGCCTGAGAGCCATGGAGCTCCGGAAGGCCAGGGCTGGATAGTGAGCCCGG
GGCTGGTGGTGCCCTGCCCTAGGCCTTCTCCTTTGACCCTGGTTTGGGGCTTGATCTTGT
GTCATGGGTACCCACGACGGGCATACTGTGGTGTGGCTCCACCTCTCGCAGATGGGAACA

37254   CATTATTCTGCCGAGTCCTTCCTGCTCACAGGTCCAGAGAGTGGACACTGGGAAAGGGT
GGCAGCTAGGACCCAGTGAACCTGGTGAGGACCTGCTCAGTGAAGGCTTCAACCCCCTGG
CAAAACCCTCCTGTAGGTGGTCCTGGTTTCTGTGTCTGTGTCTGTCTGTCCTCTGGTCTC
CTGTGTGAACTGTGACACTCTGCTTCTTGAGAACACTCAGGAGATGTCTTGCATCCTTGC
AGTTTGGCCATCCAGAGAACTTCCATGGCACCTAGGGATGGAGCCCTCACTCTTTCACCC
[T,C]
GGCACTCTGCTTCCAGGCCTGGGTGGAAGCTGTCAAAGGCAGAGTCCCCAGTGCCCCAGG
CGGCTCCAGTACTGAGCATGGTTTCTCCTCTAAGTGTCGTGCATCCATGCCCTCCTCCAC
GCAGAGGAGATCCTGAGGTGCCACCCTGAGGGCTCTGACGCCCACTCAAGATCCCCTTCTT
GCTGAGAGGCTATAGGAAGTGCCTCTTTTGGGGGGTTTCGGGAGACCCCTTGGCCCCCTTGT
CAGACACAGCCACTCTCTTGTGGATCTCGGCTGCCCGGACTTCAGGTTGGGGAGAGGGTACAA

40809   GTCGGCAAAGGAAACAGAGGAAGGACAGAGAGGTAGGGGGAAAAGAGAAATGTGCAGCAG
CTGCAGCTCTTCCAGGAACCCTGAGGATGAGGGCTGGGCAGACACATCATTAGGTAAAGG
CTTTAAATGAGGACGTGCGTGGGGAACCTAGCCCTGCAATGTGTTGTGTGTCTGACCCTG
ATATGTGCTCAGTAAATGAGTTTTATGCCACATTCTTTTGAGAAAAGAGCTTCAATATCA
TGGTGGGAACCAGAGGCCAATGATCACCCAAAATTAAAAGGCCAACCGCGTATTCGCAGC
[C,A]
GTTGTGATGGGAGGGGTTAATATTTTTATTGAAAGAGTTTCTGTGACAAATAATCCCTCT
TAAAAACCCAGTAGAAGCTGGGCGTGGTGGCTCAGGCCTGTAATCCCAGCACTTTGGGAGG
CCGAGGCGGGTGGATCACGAGGTCAGGAGATCGAGACCATCCTGGCTAACACGGTGAAAC
CCCATCTCTACTGAAAATACAAAAAATTAGCCGGGTGTGGTGGCAGGCGCCTGTAGTCCC
AGCTACTTGGGAGGTTGAGGCAGGAGAATGGCGTGAACCCGGGAGGCGGAGCTTGCAGTG

41025   TTTGAGAAAAGAGCTTCAATATCATGGTGGGAACCAGAGGCCAATGATCACCCAAAATTA
AAAGGCCAACCGCGTATTCGCAGCCGTTGTGATGGGAGGGGTTAATATTTTTATTGAAAG
AGTTTCTGTGACAAATAATCCCTCTTAAAAACCCAGTAGAAGCTGGGCGTGGTGGCTCACG
CCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCACGAGGTCAGGAGATCGAG
ACCATCCTGGCTAACACGGTGAAACCCCATCTCTACTGAAAATACAAAAAATTAGCCGGG
[T,C]
GTGGTGGCAGGCGCCTGTAGTCCCAGCTACTTGGGAGGTTGAGGCAGGAGAATGGCGTGA
ACCCGGGAGGCGGAGCTTGCAGTGAGCTGAGATTGTGCCACTGCACTCCATCCTGGGTGA
CAGAGCAAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAACCCAGTAGATAGGC
TAGGTGTGGTGGCTCACATCTGTAATCCCAGCACTTTGGGATGCTGAGGTGGGCTGATCA
CTTGAGGCCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAAACCCCCTCTCTACTAAA

FIGURE 3X

42232   GGAAACGTAGTGAGACCCCATCTCTTAAAAAAAAAAAAAAAAAAATTAGCTGAGTGTGGTGG
AACGTGCCTGTAGTCCCAGCTACTTGGGAGGCTGAGGTGGGAGGATTGCTTGAGCCCAGG
AGGCTGAGGTTACAGCCAGGATCACACCACTGCGCTCCAGCCTGGGTGACAGAGTGAGGC
TCTGTTTAAAAAAAAAAAAAAAAAAGAGAGAGAAGAAAAAAAAAGATTGGAGACAATTTGAAA
AGCCAGTAAGGAGCCAGACACAGTGGTGCGTACCTATAGTCCCAGCTACTCAGGAGGCTG
[T,C]
CGCAGGACAGAATTGCTTGAGCCCAGGAATTCGAGGCCAGCTGGGCAACATAGTGAGACC
CCCAACTCTTAAAAATGTTTTTAAATTTAAAAATAAAAAGATTTTTTAAAAGCCAGTAAA
TGACTAAATAATTATGGGAAATCTACTTAATAAACTATTCAAAAGTTATTAATTTTCATG
ACCGTAGGGATATTTTAAGTGAAAAATAAAGTGCAGAAATGTTTTATATTAAGTGAAGGA
AGTGGTATATAAAGGAGTACAGACAAGCCAGGCACGGTGGCTCACGCCTGTAATCCCAGC

50477   TTGGGACCTGAACATCAGTTCTTGGAGGCCCCCTTGTAAAACCTGCCTCAGCCTCTCCTT
TGCAAAGCCAGAAACAGGAAAGAGGGCTGGGGTCCCCACCTCTGGATGGTGCTGAGGTCT
CCAGGCTCCTGGAGTGCCTCATGCTGGCTAAGTTCTCTCTCTGGGCTCCTCCAGGGGTTCTG
TGTGCTCTTGGAGGTCCCTCTGCTAGTGGTGGCTAACTAGAGAGTCAGCAGGGGGGTGAC
TGGGAAAGAGGGAGAGGTGATGTTGCCTGCTACTCCCCTCCTTGCGGACCCTCATACCAC
[G,A]
TGACGTGGCGGCGTGGGGCCAGGAACTAGGGAAGGCAGAAGGCGGGCGCAGTGGGCAGCT
CTCTGGGCTCAGCTTGCTGAGGGGGCCTCCTGTCCTGGCTCTTTCTGGGAGACCTCATTC
TTCTGCCCATGTTCCTGCCTCACACATTCCCCGTGATGAACGCTGTGGGCGGGGCCCGGC
CTGTGCCCTCAGTCCCACAGCTCCTCTAGTGTACCTGCCCCGTGGGAACCCCATGTGGAA
AGAGCCCTCAGAACTGACAGGAATCAGGGACAGAGGCCCTTGCTGTCAGCCTCCTGGGCA

55352   TAGTAGCTCCAGGCCCCTGTGAGTGAGGTCAGATCAGTTTTGATTCCGGCACTGCTGGCA
ACATAGGAGGCGCTGTCACTGCTGGGCTCTGGACCCGTGTGGCCTGGCCCCCTGGAACATC
TTCCCCGGGATCAGGGGTCCTTGGACAGGCTGTTGTAAGGCTCGTCTGGAAGCCACAGCC
CAGGTCTGGGCACCTGCCTGGTGCCCTCAGCTGGGAGGCCTCTCTGGCAGAGGCGGCGGC
GTGGGATGTCGTCCAGTGTCCACAGCAGCCTGAGGCGAGGCGTCCCCTTGCCCCGGCTCT
[A,G]
CAGCGCCATGGGCTCGGGGCCTGTCTGGCTTGCTCGCTCACCTGCCTTGTTCTGTTTGTT
TTGGCTGCTCTGCCTTGCCCTGCCCTGCCCTGCCCTGGCTGGCTAGCTGCCCCGCTCCGC
ACTGGGAATGGCAGCTCGGTGCCTGAAGGACGGAGCTCCCGGACAGAACAGCCCCTCT
GCAGGCATGCAGCCCCAGCCTTCTCTCTGCTCCTCAGCCAGTAAGTGTGAGGGAGGCACA
TTCTGGCTTCCGTCTCCCTGGCTCGTCCTGAAGCCCCTCAGGGACCCCCCACCACAGCTGT

55914   CTCGTCCTGAAGCCCCTCAGGGACCCCCACCACAGCTGTCAGTCCCACCCACCTGCCCGT
GGTAGTAAGCTCTGGGAGCATGGCCTCTGCTGGGGGTGGGGGGTAGACTGGAGGTGCTGT
TGAGACCAGGCAGGGGCCCCTGAGTCTGGGGCCCAAAGAAATATGAGAAGTGTGGGTGGA
AAAACATGGCCTGGGATGAGGGGAGTAGAAAGCCCCCAGGATGTGCAGTGGGCCTTGCCT
CAGCGCTGAGCCAGGAAGAAGGGCAGAGTCGGAAGTCAGGTCTGTGGGGGTGGGAGTGGG
[A,G]
TGATGGGAAATCGTGACAGCGAGGAACTGTGTTGGGGATGTAGTGCTTCCTGAGTCTCA
GCATAACAGTATTAAGAGCATGGGGTCAGAGGCAAGATAGATCTGAGTTTAAATCCCAGC
TACACTGCCTTCAAGAGTGTGAAGTTTAACCTCCCAGAGCTGCAGGTTCCTTATCTGTAA
TGTGGAAATAAAATGGCACGCACCTCAGAGCCTTGTTAGATAAAAGACAAGGCAGTAGGA
AGTCTTGATACGGTGCCTCGATGGGTTATCAGTAGCTCATCCTCATATTTCTAGTTACGT

56633   TGGGGTTGGAGAGGGTGTGTGTGTGTTGTGGGTGCACACCTGCCTGCTGCTTTTGGAAGCCG
ATCGAACTCCTTGCTTCCCTTAACCTGCTGCTGCTTGCTCACCTGGAGCTGTGGCCTAGCGGG
GCTGACGGCTGTGGGGCCCCCTCCTGGATGTGCCTTTGGCTGCGCTGCCCTGTCCCAACT
GTGCTGCTTGCCTGTGCTGGCCCGGCTGGGCCGTGGTGGTGCTGTTCTAACGCTTGCAGT
TGTCTTGCAGCCTTTTGCTCCTGTGAGGAAAGGGTTGTGGCCTGGCCCCGCCCAGGGCTC
[G,A]
GGTTAGGATGAGCCCAAGCTCAACCCAAGCTCTCCCTTACCCTGGTGGCAGCCCCTGCTG
GTAGTGGCATTCCCTATAAGAGAAGCCCATGCCGGCAGGACATCACCAGCTGTCCCTTGG
CTTTGGATGGGTTGGGGAGGAGGCCTCTGGAGGGCACCACCTCTGCCTGCCTGTCAGTCT
GAGCCCTGTCTGGTTTTCCTGAGGAACACGTCCTGGCAATGAGAGCTGGTGTGAAATGTG
CAGCTTTCCCAAGCCTCGAGAGGTAAATGGAGCAGCCTCTCTCGGTACAGGCTGTCCCAAG

FIGURE 3Y